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(54) Title: ATTENUATED SALMONELLA SPI2 MUTANTS AS ANTIGEN CARRIERS (57) Abstract <p>The present invention relates to vaccines, in particular, to an attenuated gram-negative cell comprising the SPI2 gene locus, wherein at least one gene of the SPI2 locus is inactivated, wherein said inactivation results in an attenuation/reduction of virulence compared to the wild type of said cell, and to a carrier for the presentation of an antigen to a host, which carrier is said attenuated gram-negative cell, wherein said cell comprises at least one heterologous nucleic acid molecule comprising a nucleic acid sequence coding for said antigen, wherein said cell is capable of expressing said nucleic acid molecule or capable of causing the expression of said nucleic acid molecule in a target cell.</p>		

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ATTENUATED SALMONELLA SPI2 MUTANTS AS ANTIGEN CARRIERS

Description

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Background of the invention

10 In 1996, over 17 million people world-wide, mainly in developing countries, were killed by various infections. The appearance and spread of antibiotic resistances coupled with the increase in world-wide travel has led to an increasing risk for the outbreak of pandemic infections. This possibility must be taken very seriously since, for some pathogenic bacteria, the therapeutic

15 alternatives available have been reduced to a single option. Intriguingly, pathogenic bacteria have also been discovered to be a relevant factor in many chronic diseases. Stomach cancer, for example, is the second most common cancer world-wide and is directly linked with chronic *Helicobacter pylori* infections. *Chlamydia pneumoniae* has been detected in

20 arteriosclerotic plaques and recently this bacterium has been found in the diseased regions of the brain of people suffering from Alzheimer's disease. Many autoimmune diseases, such as rheumatoid arthritis, seem to have bacterial origin. *Borrelia burgdorferi* is, in addition to many other bacteria, a prominent example of an organism causing disease affecting increasing

25 numbers of people. Finally, *Nanobacteria* have been identified in the chronically diseased kidneys of patients with crystalline deposits. Other serious chronic diseases are caused by viral pathogens, the most clinically relevant are Hepatitis B and C viruses (liver cancer) and the human papilloma virus (cervical cancer).

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The increasing clinical importance of bacterial pathogens has provoked increased discussion regarding the paradigm of medicinal treatment or

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prevention as the means to handle chronic diseases. Consistently, some chronic diseases have been successfully cured by antibiotic treatment. However, as indicated above, all micro-organisms are genetically capable of rapidly generating progenies with adequate antibiotic resistances, thus
5 impeding efficient routine treatment. Conclusively, vaccines represent an excellent alternative to pharmacological drugs, and, considering the financial aspect that disease prevention is less cost-intensive than therapy, the option of vaccination is even more attractive. Therefore, the therapeutic vaccination approach has become particularly relevant, especially with
10 respect to the treatment of cancer and chronic bacterial or viral diseases.

The most frequently practised approach uses oral delivery of either inactivated pathogens (dead vaccine) or parenteral injections of a defined mixture of purified components (subunit vaccines). Most of the dead
15 vaccines are efficacious, however, the risk that the inactivation procedure was incomplete and that the vaccinee may become infected remains a problem. Furthermore, dead vaccines very often do not cover all genetic variants that appear in nature. The subunit vaccines abolish most of the disadvantages of the traditional dead vaccines. However, they require
20 technologically advanced antigen and adjuvant preparations, which makes such vaccines relatively expensive. Furthermore, the subunit vaccines are preferentially inoculated by the parenteral route, which is not the optimal route for eliciting a broad immune response. In particular, the mucosal branch of the immune system, which is the primary line of protection
25 against many pathogens, is strongly neglected by parenteral immunisations.

Another generation of vaccines is represented by live attenuated vaccines, which are based on pathogenic bacteria or viruses that have been mutated to apathogenic variants. These variants multiply *in vivo* for a limited period
30 of time before they are completely cleared by the host. Their limited prevalence in the host tissue is sufficient to adequately provoke the host immune system, which is then able to establish a protective immune

response. From the safety aspect, live attenuated bacterial vaccines are more favoured than live attenuated viral vaccines. Should a live bacterial vaccine becomes threatening for a vaccinee, the attenuated bacteria can generally be controlled by antibiotic treatment. In contrast, live viral vaccines, which use the replication apparatus of the host cell, are almost impossible to control. Live bacterial vaccines are typically administered orally and serve as excellent stimulators of the mucosal immune system. Moreover, live bacterial vaccines are also good stimulators of the systemically active immune system, namely the humoral and cellular branches. Due to these excellent immuno-stimulatory characteristics, live bacterial vaccine strains, such as *Salmonella*, are ideal carriers for expressing antigens from a heterologous pathogen. Such bivalent (or multivalent) vaccines mediate protection against two pathogens: the pathogen homologous to the carrier as well as the pathogen whose protective antigen(s) are expressed by the carrier. Although no bivalent bacterial vaccine expressing heterologous antigens is currently in use, potential carriers currently under investigation include *Bacille Calmette-Guerin* (BCG), *Salmonella* species, *Vibrio cholerae* and *Escherichia coli*.

In the attenuation process, mutations are preferentially targeted to genes that support the survival of the pathogen in the host. Initially, chemical mutation regimes were applied to the *Salmonella typhi* strain Ty2, resulting in what were thought to be perfectly attenuated pathogens capable of mediating protective immunity, in contrast to the dead homologue. However, subsequent large-scale clinical trials revealed that such strains were still not sufficiently efficacious in the prevention of typhoid fever. It appears that such strains were mutated in several genes, resulting in an over-attenuation, which adversely affects the immunogenic potential of the strain. Novel typhoid vaccine strains have been developed by the introduction of genetically defined mutations. Most of these mutations have been established in *S. typhimurium*. Infection with *S. typhimurium* causes typhoid fever-like symptoms in mice and murine salmonellosis is a well

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accepted model for human typhoid. Such vaccine strains contain mutations in proteins causing deficiencies in the biosynthesis of aromatic amino acids (e.g. *aroA*, *aroC* and *aroD*) or purines (e.g. *purA* and *purE*), in the adenylate cyclase gene (*cya*) or the cAMP receptor protein (*crp*), or possess mutations affecting the regulation of several virulence factors (*phoP* and *phoQ*). However, although a number of attenuated mutants have been generated and characterised in the mouse model with regard to their role in virulence, relatively few of them have been evaluated as vaccine carriers in humans. The reason for this is that the mutants used are either still too virulent, causing severe side effects in the host, or are not sufficiently immunogenic, due to inadequate presentation to the immune system, which requires a critical level of persistence of the vaccine strain in the host for activation.

A recent study revealed that the inactivation of individual *Salmonella* genes causing attenuation of virulence directly influences the quality of an immune response against the vaccine carrier strain. From this finding, one can conclude that it might be possible to generate a variety of differently attenuated *Salmonella* vaccine strains, each with a unique profile and individual capabilities for eliciting an immune response. With this repertoire, it might be possible to tailor a vaccine strain according to specific immunological demands. As a logical consequence, one should also be able to develop attenuated *Salmonella* vaccine strains for either prophylactic or therapeutic purposes. However, the means by which such a representative repertoire of *Salmonella* vaccine strains is obtained and further developed into an efficacious vaccine must be determined.

In cases in which a *Salmonella* vaccine strain is used as a carrier for heterologous antigens, additional parameters must be considered. Traditionally, heterologous antigens have been expressed in the *Salmonella* cytosol. In the mouse typhoid model, it was demonstrated that, when heterologous antigens are expressed at high levels in the *Salmonella* cytosol, inclusion bodies are often formed, which negatively influence the

immunogenicity of the recombinant live vaccine strain in the vaccinated host. It was concluded that the formation of inclusion bodies might be fatal for the bacterium, further decreasing vitality and increasing attenuation, and thus lowering the immunogenicity. Indeed, specific expression systems that
5 circumvent this secondary attenuation principle, e.g. the 2-phase regulated expression system, can improve the efficacy of the presentation of heterologous antigens to the host immune system.

It has been demonstrated that secretion of antigens by live attenuated
10 *Salmonella* can be superior to intracellular expression of the same antigens both in eliciting protective T-cell responses (Hess et al., 1996; Hess et al., 1997b) and in eliciting elevated levels of antigen-specific antibody (Gentschev et al., 1998). Efficiencies of HlyA-directed secretion systems, however, are usually low (30% or less of total synthesized antigen) (Hess
15 et al., 1997a; Hess et al., 1996), and the system seems to be problematical in *S.typhi* for export of heterologous antigens (Orr et al., 1999).

A similar immunological profile is induced by the two type III secretion systems, which are encoded by the *Salmonella* Pathogenicity Islands 1 and
20 2. These complex secretion machineries naturally deliver "effector proteins" into the cytosol of the infected host cell, supporting the survival of the pathogen within the host cell. By means of gene technology, the "effector proteins" can be converted into carrier vehicles for epitopes from heterologous antigens. Such chimeric "effector proteins" lose their virulent
25 character but retain their secretory character. Consequently, the chimeric "effector protein" is delivered into the lumen of the host cell, where it is appropriately processed and subsequently stimulates the cytotoxic branch of the host immune system.

30 The most abundant protein secreted by *Salmonella* is flagellin (see, for example (Hueck et al., 1995)). In *S.typhimurium*, flagellin occurs in two allelic variants, FliC or FljB, while *S.typhi* carries only the FliC gene. Flagellin

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is secreted via the flagellum-specific export (FEX) pathway (Macnab, 1996; Minamino and Macnab, 1999), which is homologous to the type III secretion pathway (Hueck, 1998). It also has been shown recently that the FEX pathway functions in secretion of non-flagella proteins in *Yersinia enterocolitica* (Young et al., 1999). Like in type III secretion, the amino terminus of FliC directs secretion. Thus, a truncated version of 183 amino terminal amino acids of FliC (full length is 495 aa) is constitutively secreted in large amounts (Kuwajima et al., 1989). In analogy to type III secretion, the effective secretion signal in FliC may be as short as 10 to 20 amino acids. The FliC or FljB secretion signals can potentially be used to secrete large quantities of a heterologous protein which can serve as an antigen in heterologous vaccination. It is likely that the amount of secreted antigen can be even further increased in regulatory mutants affecting the expression of flagella biosynthesis genes (Macnab, 1996; Schmitt et al., 1996) or by using recombinant promoters to drive expression of the flagellin gene.

Secretion via the FEX pathway can allow the delivery of large amounts of antigen into the *Salmonella*-containing phagosome for early and efficient antigen processing and antigen presentation to the host immune system. Especially the MHC class II dependent branch of the host immune system is strongly supported by the FEX pathway mediated antigen delivery.

The other known export machineries and surface display systems of Gram-negative bacteria can be also applied to bacterial vaccine carriers such as *Salmonella*. In general, a good immune response is achieved when the antigen is presented on the *Salmonella* surface. However, as little is known about the immunological consequence of such antigen presentation systems, further experimental work is needed.

Additional immuno-modulatory effects can be achieved when environmentally regulated *Salmonella* promoters are used for the expression of heterologous antigens. For instance, the expression of a heterologous

gene in a *Salmonella* carrier strain under control of the *in vivo* regulated stress response *htrA* gene promoter resulted in a stronger immune response than was obtained when under control of the anaerobically inducible promoter of the *nirB* gene.

5

According to a first aspect, the present invention relates to an isolated nucleic acid molecule comprising a nucleic acid sequence comprising at least 50 nucleotides a) of the nucleic acid sequence of one of Figs.21A, B, b) of an allele of the nucleic acid sequence of one of Figs.21A, B or c) of
10 a nucleic acid sequence which under stringent conditions hybridizes with the nucleic acid sequence of one of Figs. 21A, B.

Stringent hybridization conditions in the sense of the present invention are defined as those described by Sambrook et al., Molecular Cloning, A
15 Laboratory Manual, Cold Spring Harbor Laboratory Press (1989), 1.101-1.104. According to this, hybridization under stringent conditions means that a positive hybridization signal is still observed after washing for 1 hour with 1 x SSC buffer and 0.1 % SDS at 55°C, preferably at 62°C and most preferably at 68°C, in particular, for 1 hour in 0.2 x SSC buffer and 0.1 %
20 SDS at 55°C, preferably at 62°C and most preferably at 68°C.

In particular, the present invention relates to such a nucleic acid molecule which comprises the complete coding regions or parts thereof of the genes *ssaD*, *ssaE*, *sseA*, *sseB*, *sscA*, *sseC*, *sseD*, *sseE*, *sscB*, *sseF*, *sseG*, *ssaG*,
25 *ssaH*, *ssaE*, *ssaJ*, *ssrA* and *ssrB*. The invention pertains also to such nucleic acids, wherein at least one coding region of said genes is functionally deleted.

In one embodiment, the nucleic acid molecule comprises an insertion
30 cassette to facilitate the insertion of a heterologous nucleic acid molecule by transposon or phage mediated mechanism.

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Furthermore, said nucleic acid molecules can comprise at least one heterologous nucleic acid molecule. In this case the heterologous nucleic acid molecule may be fused 5' or 3', inserted or deletion-inserted to the inventive nucleic acid molecule. By the term "deletion-inserted" it is understood that the insertion of the heterologous nucleic acid molecule is associated with a concurrent deletion of parts of the inventive nucleic acid molecule. Preferably, the nucleic acid molecule is inserted or deletion-inserted and in one preferred embodiment the heterologous nucleic acid molecule is flanked 5' and 3' by sequences of the nucleic acid molecule according to the invention, wherein each of said sequences has a length of at least 50 nucleotides, preferably 200-250 nucleotides.

Preferred, the heterologous nucleic acid molecule codes for a polypeptide or peptide, more preferred it codes for a bacterial or viral antigen or a homologue thereof or for a tumor antigen.

It is preferred that the nucleic acid molecule also comprises at least one gene expression cassette to allow for efficient expression of the heterologous nucleic acid molecule. Such gene expression cassette usually comprises elements such as promoters and/or enhancers which improve the expression of the heterologous nucleic molecule acids. Usually, such gene expression cassette comprises elements for the termination of transcription. The presence of transcription terminators, however, may be not preferred in cases where the heterologous nucleic acid molecule is to be transcribed together with other genes into a cistronic mRNA.

The nucleic acid molecule, one or more selective marker cassettes and one or more transactivator cassettes and optionally invertase cassettes for allowing the expression of the heterologous nucleic acid molecules in a one-phase system or a two-phase system. Furthermore, sequences may be present which code for a polypeptide or peptide-targeting domain and, thus, allow for the targeting of the expression product of the heterologous nucleic

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acid molecule to a predetermined cell compartment such as cytosol, periplasma or outer membrane, or the secretion of said expression product, or which code for an immunostimulatory domain.

5 According to another aspect, the invention relates to a recombinant vector which comprises the nucleic acid molecule described above. Another aspect of the invention pertains to a cell comprising a modified inventive nucleic acid molecule as described above by insertion of a heterologous sequence or the recombinant vector. The cell may be a prokaryotic cell such as a
10 gram-negative cell, e.g. a Salmonella cell, or it can be a eukaryotic cell such as a mammalian cell, e.g. a human cell, and, in particular, a macrophage.

According to a still further aspect, the present invention relates to a peptide or polypeptide comprising a peptide sequence comprising at least 20 amino
15 acids a) of the sequence of one of Figs. 23A-Q, or b) of a sequence which is 60%, preferred 65% and more preferred 70% homologous to the sequence of one of Figs. 23A-Q. In particular, the invention relates to a polypeptide comprising the sequence a) of one of Figs. 23A-Q, or b) which is 60%, preferred 65% and more preferred 70% homologous to the
20 sequence of one of Figs. 23A-Q.

Percent (%) homology are determined according to the following equation:

$$25 \quad H = \frac{n}{L} \times 100$$

wherein H are % homology, L is the length of the basic sequence and n is the number of nucleotide or amino acid differences of a sequence to the
30 given basic sequence.

Another aspect of the present invention relates to an antibody which is directed against an epitope which is comprised of the aforementioned peptide or polypeptide. The antibody may be polyclonal or monoclonal.

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Methods for producing such an antibody are known to the person skilled in the art.

5 A further aspect of the present invention relates to a fusion protein comprising the polypeptide according to any one of the claims 17 and 18 having inserted or deletion-inserted or being fused C- or NH₂-terminally with at least one heterologous polypeptide. The heterologous polypeptide preferred is an antigen, more preferred a bacterial or viral antigen or a tumor antigen.

10

The present invention furthermore provides instructions for the development of a variety of potential live *Salmonella* vaccine strains with different attenuation levels, which subsequently serve as platforms for the development of recombinant live *Salmonella* vaccine carrier strains that
15 express antigens from heterologous pathogens, thus serving as multivalent vaccines. Such recombinant live *Salmonella* vaccine carriers are equipped with modules comprising variable gene cassettes that regulate the expression of heterologous antigens in *Salmonella* and determine presentation of the heterologous antigens to the host immune system. By
20 combinations of both systems, differently attenuated live *Salmonella* vaccine strains and variable gene cassettes, a variety of recombinant live vaccine carrier strains can be generated that have, due to their variable immunogenic characteristics, a broad application spectrum for both prophylactic and therapeutic use. The basic attenuation principle originates
25 from novel mutations in the *Salmonella* Pathogenicity Island 2 (SPI2) gene locus. Additional mutations, which can be used either alone or in combination with mutations in *sse* or SPI-2 genes or in combination with the *aroA* mutation for optimal attenuation of live vaccine carrier strains, have been reported recently (Heithoff et al., 1999; Valentine et al., 1998).
30 By combination of the individual mutations in the SPI-2 gene locus with each other and with other known attenuating gene mutations, such as *aroA*, etc., a broad repertoire of attenuation and immunogenicity can be

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achieved. Different expression cassettes can be introduced on these platforms, allowing further modulation of the immune response directed against the heterologous antigens. Finally, a library of individual recombinant live *Salmonella* vaccine carrier strains is generated, covering
5 a broad spectrum of immuno-stimulatory potential, from which a genuine live vaccine strain can be tailored for the optimal protection or treatment of humans and/or animals against specific pathogens or disease.

Thus, in a further aspect, the present invention is an attenuated gram-
10 negative cell comprising the SPI2 gene locus, wherein at least one gene of the SPI2 locus is inactivated, wherein said inactivation results in an attenuation/reduction of virulence compared to the wild type of said cell.

Genes present in the *Salmonella* pathogenicity island 2 that encode for a
15 variety of proteins involved in type III secretion and those that are required for systemic spread and survival within phagocytic cells are ideal candidates for attenuation of pathogenic *Salmonella* ssp.

Several gram-negative bacterial pathogens secrete certain virulence proteins
20 via specialised type III secretion systems. Virulence factors enable pathogenic bacteria to colonise a niche in the host despite specific attacks of the immune system. The type III secretion systems comprise a large number of proteins required to transfer specific effector proteins into eukaryotic host cells in a contact-dependent manner, thus they have also
25 been called contact-dependent secretory systems. Although several components of the secretion system apparatus show evolutionary and functional conservation across bacterial species, the effector proteins are less well conserved and have different functions. The *Yersinia* effectors YpkA and YopH have threonine/serine kinase and tyrosine phosphatase
30 activities, respectively. The actions of these and other Yops inhibit bacterial phagocytosis by host cells, which is thought to enable extracellular bacterial proliferation. The *Shigella* Ipa proteins, secreted by the *mxi/spa* type III

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secretion system, promote entry of this bacterium into epithelial cells. EspA, EspB and EspD, encoded by the locus of enterocyte effacement (LEE) of enteropathogenic *Escherichia coli* (EPEC) are required for translocation of proteins that cause cytoskeletal rearrangements and the formation of pedestal-like structures on the host cell surface.

For the purposes of the present invention an "gram-negative cell comprising the SPI2 gene locus" is a cell having a gene locus that harbors genes required for the systemic spread and survival within phagocytic cells and, thus, is a homologue or functional equivalent of the SPI2 locus from *Salmonella*. Preferred, the inventive attenuated gram-negative cell is an Enterobacteriaceae cell, more preferred, a *Salmonella* cell, a *Shigella* cell or a *Vibrio* cell. In general, cells having a broad host range are preferred. Typical hosts are mammals, e.g. man, and birds, e.g. chicken. *Salmonella* cells are more preferred, and particularly preferred is *Salmonella* serotype typhimurium Definitive Type 104 (DT 104).

Salmonella typhimurium is unusual in that it contains two type III secretion systems for virulence determinants. The first controls bacterial invasion of epithelial cells, and is encoded by genes within a 40kb pathogenicity island (SPI1). The other is encoded by genes within a second 40kb pathogenicity island (SPI2) and is required for systemic growth of this pathogen within its host. The genes located on pathogenicity island SPI1 are mainly responsible for early steps of the infection process, the invasion of non-phagocytic host cells by the bacterium. For most of the SPI1 genes, mutations result in a reduced invasiveness *in vitro*. However, mutants that are defective in invasion are not necessarily avirulent; studies in mice demonstrated that, while these mutations in SPI1 genes significantly reduced virulence upon delivery by the oral route, they had no influence on virulence following an intraperitoneal route of infection. Taken together, these results indicate that mutations in genes within the pathogenicity island SPI1 do not abolish systemic infection and are therefore not very useful for the development of

a safe, attenuated *Salmonella* carrier strain. In comparison, virulence studies of SPI2 mutants have shown them to be attenuated by at least five orders of magnitude compared with the wild-type strain after both oral and intraperitoneal inoculation of mice.

5

Many of the genes encoding components of the SPI2 secretion system are located in a 25kb segment of SPI2. SPI2 contains genes for a type III secretion apparatus (*ssa*) and a two component regulatory system (*ssr*), as well as candidate genes for a set of secreted effectors (*sse*) and their specific chaperones (*ssc*). On the basis of similarities with genes present in other bacterial pathogens, the first 13 genes within the *ssaK/U* operon and *ssaJ* encode components of the secretion system apparatus. A number of additional genes, including *ssaC* (orf 11 in Shea *et al.*, 1996; *spiA* in Ochman *et al.*, 1996) and *ssrA* (orf 12 in Shea *et al.*, 1996; *spiR* in Ochman *et al.*, 1996), which encode a secretion system apparatus protein and a two component regulatory protein, respectively, are found in a region approximately 8kb from *ssaJ*.

10
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Preferably, the inventive attenuated gram-negative cell has inactivated at least one gene selected from effector (*sse*) gene secretion apparatus (*ssa*) genes, chaperon (*ssc*) genes and regulation (*ssr*) genes. More preferably, the at least one inactivated gene is an *sse*, *ssc* and/or *ssr* gene, even more preferred is an *sse* and/or *ssc* gene.

20

As far as the *sse* genes are affected by the inactivation, the inactivated gene is preferably *sseC*, *sseD*, *sseE* or a combination thereof. As far as the *ssr* genes are affected by the inactivation, preferably at least *ssrB* is inactivated. As far as the *ssc* genes are affected by the inactivation, preferably at least *sscB* is inactivated.

25

30

The inactivation of said gene of the SPI2 locus (or functional homologue thereof in cells other than *Salmonella*) is effected by a mutation which may

comprise deletion. Preferred are deletions of at least six nucleotides, and more preferred is a deletion of the partial and, in particular, the complete coding sequence for said gene. The mutation may also comprise the insertion of a heterologous nucleic acid molecule into said gene to be
5 inactivated or a combination of deletion and insertion.

Pathogenic *Salmonella* ssp. serve a basis for the construction of a panel of different live *Salmonella* vaccine prototypes generated by gradual attenuations accomplished through the introduction of defined SPI2 gene
10 locus mutations. Each resulting individual live *Salmonella* vaccine prototype is further transformed into a multivalent recombinant vaccine by the introduction of exchangeable DNA modules carrying (1) genetically engineered genes from heterologous pathogens and (2) adequate expression systems executing efficacious antigen presentation to the host immune
15 system. In concert, these features elicit a specific immune response that either protects vaccinated hosts against subsequently invading *Salmonella* and/or other pathogens (prophylactic vaccination) or eliminates persistent pathogens, such as *Helicobacter pylori* (therapeutic vaccination).

Pathogenic *Salmonella* ssp. are gradually attenuated by mutations in individual virulence genes that are part of the SPI2 gene locus, e.g. an *sse* gene coding for an effector protein, such as *sseC*, *sseD* or *sseE*, or an *ssc* gene, such as *sscB*, coding for a chaperone, or an *ssr* gene, such as *ssrB*,
20 coding for a regulator. Individual mutation of each of these genes leads to a unique individual grade of attenuation, which, in turn, effects a characteristic immune response at the mucosal, humoral and cellular levels. The individual grade of attenuation can be moderately increased by combinations of at least two gene mutations within the SPI2 gene locus or by combination with a mutation in another *Salmonella* gene known to
25 attenuate virulence, e.g. an *aro* gene, such as *aroA*. A stronger grade of attenuation is achieved by mutation of a virulence gene that is part of a polycistronic gene cluster encoding several virulence factors, such as the
30

transcriptional unit comprising the *sseC*, *sseD*, *sseE* and *sscB* genes, such that the mutation exerts a polar effect, disrupting expression of the following genes. The grade of attenuation may directly depend on the number of virulence genes that are affected by the polar mutation as well as their individual characteristics. Finally, the strongest attenuation is achieved when regulatory genes, such as *ssrB*, are mutated. Again, each mode of attenuation of a *Salmonella* *ssp.* leads to the generation of a live *Salmonella* vaccine strain that evokes an immune response at the mucosal, humoral and cellular levels that is characteristic for the type and/or combination of attenuating mutations present in that strain. The panel of differently attenuated live *Salmonella* vaccine strains that is generated represents a pool of potential carrier strains from which that carrier can be selected that provokes the most efficacious immune response for either the prevention or eradication of disease in conjunction with the heterologous antigens that are expressed.

Mutations leading to attenuation of the indicated *Salmonella* virulence genes are preferentially introduced by recombinant DNA technology as defined deletions that either completely delete the selected virulence gene or result in a truncated gene encoding an inactive virulence factor. In both cases, the mutation involves a single gene and does not affect expression of neighbouring genes (non-polar mutation). An insertional mutation in one of the indicated virulence genes is preferred when the selected gene is part of a polycistronic virulence gene cluster and all of the following virulence genes are included in the attenuation process (polar mutation). Insertional mutations with non-polar effects are in general restricted to genes that are either singly transcribed or are localised at the end of a polycistronic cluster, such as *ssrB*. However, other attenuating mutations can arise spontaneously, by chemical, energy or other forms of physical mutagenesis or as a result of mating or other forms of genetic exchange.

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Thus, the mutation which results in the preparation of the inventive attenuated gram-negative cell may be a polar or non-polar mutation. Furthermore, the grade of attenuation may be modified by inactivating an additional gene outside of the SPI2 locus, for example, another virulence
5 gene or a gene that is involved in the biosynthesis of a metabolite or a precursor thereof such as the aro genes, in particular, aroA, or any other suitable gene such as superoxide dismutase (SOD).

The attenuated cell according to the invention may furthermore comprise
10 elements which facilitate the detection of said cell and/or the expression of an inserted heterologous nucleic acid molecule. An example of an element which facilitates the detection of the attenuated cell is a selective marker cassette, in particular, a selective marker cassette which is capable of conferring antibiotic resistance to the cell. In one embodiment, the selective
15 marker cassette confers an antibiotic resistance for an antibiotic which is not used for therapy in a mammal. Examples of elements which facilitate the expression of a heterologous nucleic acid molecule are a gene expression cassette which may comprise one or more promoter, enhancer, optionally transcription terminator or a combination thereof, a transactivator cassette,
20 an invertase cassette for 1-phase or 2-phase expression of a heterologous nucleic acid. An example of an element which facilitates the insertion of a heterologous nucleic acid molecule is an insertion cassette.

In another aspect, the invention provides a carrier for the presentation of an
25 antigen to a host, which carrier is an attenuated gram-negative cell according to any one of the claims 22 to 49, wherein said cell comprises at least one heterologous nucleic acid molecule comprising a nucleic acid sequence coding for said antigen, wherein said cell is capable of expressing said nucleic acid molecule or capable of causing the expression of said
30 nucleic acid molecule in a target cell.

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Preferably, said nucleic acid molecules comprises a nucleic acid sequence coding for a bacterial or viral antigen or for a tumor antigen. Examples of bacterial antigens are antigens from *Helicobacter pylori*, *Chlamydia pneumoniae*, *Borrelia burgdorferi* and *Nanobacteria*. Examples of viral
5 antigens are antigens from Hepatitis virus, e.g. Hepatitis B and C, human papilloma virus and Herpes virus. The heterologous nucleic acid molecule may comprise a nucleic acid sequence which codes for at least one polypeptide or peptide-targeting domain and/or immunostimulatory domain. Thus, the expression product of said heterologous nucleic acid molecule
10 may be targeted specifically to predetermined compartments such as periplasma, outer membrane, etc. The heterologous nucleic acid molecule may code for a fusion protein.

According to one embodiment the heterologous nucleic acid molecule is
15 inserted into the SPI2 locus, preferred, into an sse gene and, more preferred, into sseC, sseD and/or sseE, in particular, sseC.

The insertion may be a polar insertion or an unpolar insertion. Generally, the introduction of an unpolar insertion is preferred, since it allows for the
20 expression of the remaining genes of a polycistronic gene cluster, which can be used for the generation of carriers having different grades of attenuation.

Attenuated live *Salmonella* vaccines are used as carriers for specific
25 antigens from heterologous pathogens, e.g. *Helicobacter*, etc., thus acting as a multivalent vaccine. The heterologous antigens are provided by a gene expression cassette (GEC) that is inserted by genetic engineering into the genome of an attenuated *Salmonella* strain. Preferentially, insertion of the gene expression cassette is targeted to one of the indicated virulence
30 genes, thereby causing an insertional mutation as described in previous paragraph. In another application form, expression of the heterologous genes in the gene expression cassette is regulated by trans-acting factors

encoded by a trans-activator cassette (TC) or an invertase cassette performing a 2-phase variable expression mode. Preferentially, the insertion of the trans-activator cassette is targeted to a second chosen virulence gene, which is then inactivated. Alternatively, the gene expression cassette
5 or the trans-activator cassette or the invertase cassette can be introduced into the *Salmonella* genome by transposon-mediated insertion, which has no attenuation effect.

The principles of genetic engineering are required to generate either deletion
10 or insertional mutations in *Salmonella* virulence genes. Generally, a suicide plasmid carrying a mutated virulence gene cassette containing a selective marker cassette (SMC) either alone or in combination with a gene expression cassette or a trans-activator cassette or the invertase cassette is introduced into the receptor *Salmonella* strain by conjugation. The original
15 virulence gene is replaced with the mutated virulence gene cassette via homologous recombination, and the suicide plasmid, unable to replicate in the *Salmonella* receptor strain, becomes rapidly depleted. Successfully recombined *Salmonella* can be selected based on properties (such as, but not limited to, antibiotic resistance) conferred by the product of the gene(s)
20 within the selective marker cassette. The mutated virulence gene cassette comprises DNA sequences that are homologous to the genome of the receptor *Salmonella* strain where the original virulence gene is localised. In the case where the original virulence gene is to be completely deleted, only those genomic DNA sequences that border the original virulence gene
25 (indicated as flanking regions) are included in the mutated virulence gene cassette. The general architecture of a mutated virulence gene cassette includes at each end a DNA sequence of at least 50 nucleotides, ideally 200 - 250 nucleotides, that is homologous to the genome segment where the original virulence gene is localised. These DNA sequences flank a selective
30 marker cassette and the other cassettes, such as the gene expression cassette (GEC) or the trans-activator cassette (TC) or the invertase cassette. As indicated above, these cassettes are used to generate

insertional mutations which disrupt original gene expression. For in-frame deletions, a selective marker cassette is preferentially used.

The selective marker cassette (SMC) principally consists of a gene
5 mediating resistance to an antibioticum which is able to inactivate the
receptor *Salmonella* strain but which is actually not used in the treatment
of Salmonellosis. Alternatively, another selectable marker can be used. The
selective marker cassette is inserted in-frame in the targeted virulence gene
and, consequently, the expression of the marker gene is under the control
10 of the virulence gene promoter. Alternatively, the cassette is inserted within
a polycistronic transcriptional unit, in which case the marker gene is under
control of the promoter for this unit. In another application, the selective
marker gene is under control of its own promoter; in this case a
transcriptional terminator is included downstream of the gene. The selective
15 marker is needed to indicate the successful insertion of the mutated
virulence gene cassette into the genome of the receptor *Salmonella* strain.
Furthermore, the antibiotic resistance marker is needed to facilitate the pre-
clinical immunological assessment of the various attenuated *Salmonella*
strains. In another application form, the selective marker is flanked by direct
20 repeats, which, in the absence of selective pressure, lead to the
recombinatorial excision of the selective marker cassette from the genome,
leaving the short sequence of the direct repeat. Alternatively, the selective
marker cassette can be completely removed by recombinant DNA
technology. Firstly, the selective marker cassette is removed by adequate
25 restriction endonuclease from the original mutated virulence gene cassette
on the suicide plasmid leaving the flanking region sequences which are
homologous to the *Salmonella* genome. The suicide plasmid is then
transferred into the attenuated receptor *Salmonella* strain by conjugation
where the SMC-depleted mutated virulence gene cassette replaces the
30 SMC-carrying mutated virulence gene cassette by recombination. After
removal of the selective marker, the attenuated *Salmonella* strain is free for

the application in humans. Transcriptional terminator sequences are generally included in the cassettes when polar mutations are established.

The gene expression cassette (GEC) comprises elements that allow, facilitate or improve the expression of a gene. In a functional mode the gene expression cassette additionally comprises one or more gene expression units derived from either complete genes from a heterologous source or fragments thereof, with a minimal size of an epitope. Multiple gene expression units are preferentially organised as a concatemeric structure.

The genes or gene fragments are further genetically engineered, such that the resulting proteins or fusion proteins are expressed in the cytosol, in the periplasm, surface displayed or secreted. Furthermore the genes or gene fragments can be fused with DNA sequences encoding immunologically reactive protein portions, e.g. cytokines or attenuated bacterial toxins. The genes or gene fragments are either controlled in a one-phase mode from a promoter within the gene expression cassette or in a 2-phase mode or indirectly by a trans-activator cassette (TC). In the one-phase mode the promoter is preferentially a *Salmonella* promoter that is activated, i.e. induced, by environmental signals but also constitutive promoters of different strength can be used. In the 2-phase mode, the expression of the gene cassette is controlled by an invertase that derived from an invertase cassette. The invertase catalyses the inversion of a DNA segment comprising the gene cassette. The DNA segment is flanked on each end by an inverted repeat which is the specific substrate for the invertase finally causing two orientation of the gene cassette with respect to the gene expression cassette promoter. In the ON-orientation the gene cassette is correctly placed allowing transcription of the gene cassette. In OFF, the orientation of the gene cassette is incorrect and no transcription occurs. The invertase cassette comprises of an invertase that is controlled by a constitutive promoter or a *Salmonella* promoter induced or derepressed by environmental signals.

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Heterologous antigens encoded within the gene expression cassette can be expressed under the control of a promoter, e.g. a tissue-specific promoter, which may be constitutive or inducible. The expression can be activated in a target cell, whereby a signal is transmitted from the target cell to the interior of the *Salmonella* cell, which signal induces the expression. The target cell, for example, can be a macrophage. The expression product may comprise a targeting domain or immunostimulatory domain, e.g. in the form of a fusion protein. The heterologous protein itself also may be a fusion protein. The heterologous antigens can be optionally expressed as cytosolic, periplasmic, surface displayed or secretory proteins or fusion proteins in order to achieve an efficacious immune response. The antigen encoding sequences may be fused to accessory sequences that direct the proteins to the periplasm or outer membrane of the *Salmonella* cell or into the extracellular milieu. If the heterologous polypeptides are secreted, secretion can occur using a type III secretion system. Secretion by the SPI2 type III secretion system is suitable. Proteins that are destined for the cytosolic compartment of the *Salmonella* do not need accessory sequences, in this case, naturally occurring accessory sequences must be removed from the genes encoding such antigens.

20

The accessory sequences for the periplasmatic compartment of *Salmonella* comprise a DNA sequence deduced from the amino-terminally localised signal peptide of a heterologous protein naturally translocated via the general secretion pathway, e.g. CtxA, etc.

25

The accessory sequences for the outer membrane compartment of *Salmonella* preferentially comprise DNA sequences deduced from the functionally relevant portions of a type IV secretory (autotransporter) protein, e.g. AIDA or IgA protease. The appropriate fusion protein contains an amino-terminally localised signal peptide and, at the carboxy-terminus, a β -barrel shaped trans-membrane domain to which the foreign passenger

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protein is coupled via a spacer that anchors the passenger protein to the bacterial surface.

The accessory sequences for secretion into the extracellular milieu comprise DNA sequences deduced from proteins naturally secreted by the type III secretion system. In a generally functional fusion protein, the heterologous antigen is fused in the centre of a protein naturally secreted by the type III pathway or at the carboxy-terminal end of the respective protein.

10 The transactivator cassettes (TC) provide activators which generally improve expression of the heterologous antigens encoded by the various gene expression cassettes. Such activators either directly (RNA polymerase) or indirectly (transcriptional activator) act on the transcription level in a highly specific order. Preferentially, the expression of such activators are controlled by *Salmonella* promoters which are induced *in vivo* by environmental signals. In another application form the synthesis of the activator within the transactivator cassette is regulated in a 2-phase mode. The invertase expressed by the invertase cassette places the activator encoding DNA fragment in two orientations with respect to the transcriptional promoter. In the ON-orientation the activator gene is in the correct transcriptional order. In the OFF-modus the activator is incorrectly orientated and no expression occurs.

In the simple system, the gene product of the transactivator cassette exerts its effect directly on the promoter present in the gene expression cassette, directly activating or de-repressing expression of the heterologous gene. In the complex system, activation of the promoter in the heterologous gene expression cassette is dependent upon two or more interacting factors, at least one of which (encoded in the transactivator cassette) may be regulated by external signals. Further complexity is found in cascade systems, in which the external signal does not directly exert its effect on the transactivator cassette, but rather through a multi-step process, or in

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which the gene product of the transactivator cassette does not directly exert its effect on the heterologous gene expression cassette, but rather through a multi-step process.

5 According to still another aspect, the present invention is an attenuated gram-negative cell comprising the SPI2 gene locus, characterized by a lack of at least one SPI2 polypeptide, wherein said lack results in an attenuation/reduction of virulence compared to the wild type of said cell. Preferably, said missing SPI2 polypeptide is one or more effector
10 polypeptide, secretion apparatus polypeptide, chaperon polypeptide or regulatory polypeptide. Furthermore, said attenuated cell may be a carrier which then is characterized by the presence of at least one heterologous peptide or polypeptide having immunogenic properties.

15 A further aspect of the present invention is a pharmaceutical composition which comprises as an active agent an immunologically protective living vaccine which is an attenuated gram-negative cell or carrier according to the invention. The pharmaceutical composition will comprise additives such as pharmaceutically acceptable diluents, carriers and/or adjuvants. These
20 additives are known to the person skilled in the art. Usually, the composition will be administered to a patient via a mucosa surface or via or via the parenteral route.

Further aspects of the present invention include a method for the
25 preparation of a living vaccine, which comprises providing a living gram-negative cell comprising the SPI2 locus and inactivating at least one gene of the SPI2 locus to obtain an attenuated gram-negative cell of the invention, and optionally inserting at least one heterologous nucleic acid molecule coding for an antigen to obtain a carrier according to the
30 invention. A further aspect pertains to a method for the preparation of a living vaccine composition comprising formulating an attenuated cell or a carrier according to the invention in a pharmaceutically effective amount

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together with pharmaceutically acceptable diluents, carriers and/or adjuvants. A further aspect of the invention relates to a method for the detection of an attenuated cell or a carrier according to the invention, comprising providing a sample containing said cell and detecting a specific property not present in a wild type cell. Methods for detecting a specific property of the attenuated cell or carrier, which is not present in wild type, are known to the person skilled in the art. For example, if this specific property of the attenuated cell comprises a deletion of one or more parts of the SPI2 locus, then the presence of said cell can be detected by providing a pair of specific primers which are complementary to sequences flanking this deletion and amplifying a fragment of specific length using amplification methods such as PCR. Methods for detecting the presence of an inventive carrier comprise PCR amplification of an inserted fragment or a fragment spanning the insertion boundary, hybridization methods or the detection of the heterologous expression product or of a selective marker.

A further aspect of the invention is a method for establishing a library of attenuated gram-negative cells or carriers, respectively, according to the invention. The method comprises the preparation of attenuated recombinant vaccine strains, each having a different mutation in the SPI2 locus which results in a different degree of attenuation. The pathogenicity or virulence potential of said strains can then be determined using known methods such as determination of the LD50, and the strains are rated according to the different pathogenicities, i.e. a different grade of attenuation. Preferably, the method comprises also the determination of other parameters of interest such as the immunogenicity or the immuno-stimulatory response raised in a host. Methods for determining the immuno-stimulatory potential are known to the person skilled in the art and some of them are described in Example 6. Preferably, the immuno-stimulatory potential of the inventive attenuated cells or carriers is determined at humoral, cellular and/or mucosal level. In this way it is possible to establish a library of attenuated cells or carriers having a predetermined attenuation degree and predetermined

immuno-stimulatory properties. Thus, for each application, the strain having the desired properties can be selected specifically. For example, it will be usually preferred to select a strong attenuated strain for administration to patients which receive immunosuppressive drugs.

5

In a similar way, the invention allows for the establishment of libraries of attenuated carriers having defined pathogenicities and optionally immunogenicities. The establishment of a carrier library additionally will comprise the determination of the antigen presentation of said carrier strains to a host, whereby a panel of different carriers strains will be obtained having defined properties with respect to pathogenicity, immuno-stimulatory potential of carrier antigens and immuno-stimulatory potential of the heterologous antigen.

15

Another aspect of the invention is the use of the attenuated cell or carrier according to the invention for the preparation of a drug for the preventive or therapeutic treatment of an acute or chronic disease caused essentially by a bacterium or virus. For example, for the prevention or treatment of a *Salmonella* infection one will administer an attenuated *Salmonella* cell to raise the immune response of an affected patient. Similarly, a carrier according to the invention may be used for the preparation of a drug for the preventive or therapeutic treatment of a tumor.

25

The individual immuno-protective potential of each of the established recombinant *Salmonella* vaccine strains is determined in a mouse model using a pathogenic *Salmonella typhimurium* as the challenge strain.

30

- Determination of the virulence potential of the recombinant *Salmonella* vaccine strain: (1) Competitive index or LD50; (2) Systemic prevalence in blood, liver and spleen strictly excluded.
- Determination of the immuno-stimulatory potential of the carrier strain with a cytosolically expressed heterologous test antigen: (1)

- Single oral immunisation and subsequent evaluation of the short- and long-term immune response: (a) analysis of the humoral immune response profile, (b) analysis of the mucosal immune response profile, (c) analysis of the cellular immune response profile; (2)
- 5 Multiple oral immunisations and subsequent evaluation of the short- and long-term immune response: (a) analysis of the humoral immune response profile, (b) analysis of the mucosal immune response profile, (c) analysis of the cellular immune response profile.
- Determination of the immuno-stimulatory potential of the carrier
- 10 strain for the delivery of heterologous DNA (DNA vaccination).

Preferentially, the *Salmonella* acceptor strain has a broad host range, exhibiting significant pathogenicity in both animals and humans. Ideally, this is a *Salmonella* strain that is strongly pathogenic for mice, such as *S.*

15 *typhimurium*. After successful development of the recombinant *Salmonella* vaccine strain, the strain is directly applicable for use in both animals and humans. If such an ideal *Salmonella* acceptor strain is not satisfactory for the respective host, other host-specific *Salmonella* must be selected, such as *S. typhi* for humans.

20

Other aspects of the invention relate to the use of a nucleic acid molecule as shown in Fig. 21A or B or one of the Figs. 22A-Q, optionally modified as described hereinabove or of a vector as described hereinabove for the preparation of an attenuated cell, a living vaccine or a carrier for the

25 presentation of an antigen to a host and to the use of the *Salmonella* SPI2 locus for the preparation of an attenuated cell, a living vaccine or preferably a carrier for the presentation of an antigen to a host. In this context the term "Salmonella SPI2 locus" refers to any nucleic acid sequence, coding or not coding, and to the expression product of coding sequences.

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A still further aspect of the present invention is the use of a virulence gene locus of a gram-negative cell for the preparation of a carrier for the presentation of an antigen to a host.

5 Another aspect of the invention relates to a method of therapeutically or prophylactically vaccinating an animal, e.g. a mammal, e.g. a human, against a chronic disease caused primarily by a infectious organism including preparation and administering a vaccine of the invention.

10 Still another aspect of the present invention is an isolated nucleic acid molecule comprising a nucleic acid of at least 100 nucleotides a) of the nucleic acid sequence of one of Figs.24A, B, b) of a nucleic acid sequence which under stringent conditions hybridizes with the nucleic acid sequence of one of Figs.24A, B.

15

In particular, said aspect relates to said nucleic acid molecule which is capable of inducing the expression of a nucleic acid sequence coding for a peptide or polypeptide operatively linked to said nucleic acid molecule.

20 The in vivo inducible promoter Pivi comprises a DNA fragment which carries sequences for an operator and a transcriptional promoter. Such in vivo inducible promoter can be identified by applying an adequate reporter gene approach. Two of such in vivo inducible promoters have been identified within the SPI2 locus which initiate expression of the ssaBCDE operon (promoter A2) and the sseABsscAsseCDEsscBsseFG operon (promoter B),
25 respectively. These promoters are induced by a regulative system comprising the ssrA and ssrB gene products. This regulative system is part of the SPI2 locus responsible for the activation of additional SPI2 locus genes. The regulative system is activated in macrophages by environmental

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signal(s) via sensor protein SsrA. The SsrB protein finally binds at a defined DNA sequence which initiates transcription through the RNA polymerase.

In an application form the DNA fragment comprising operator/promoter sequences is inserted in front of an invertase gene or an activator gene or a gene expression cassette, thereby executing an in vivo inducible expression in bacteria carrying at least the *ssrA* and *ssrB* genes or the complete SPI2 locus.

Thus, in a further aspect, the invention relates to an expression system for the in vivo inducible expression of a heterologous nucleic acid in a target cell, comprising a carrier cell for said heterologous nucleic acid, wherein said carrier cell comprises (a) a polypeptide having the amino acid sequence shown in Fig.23P (*ssrA*) or a functional homologue thereof, (b) a polypeptide having the amino acid sequence shown in Fig.23Q (*ssrB*) or a functional homologue thereof, and (c) the nucleic acid molecule of one of Figs.24A, B or a functional homologue thereof, as described above.

The target cell may be any suitable cell but preferably it is a macrophage.

The carrier cell preferably is a *Salmonella* cell. The target cell may also comprise one or more of the elements described above such as selective marker cassettes, gene expression cassettes, transactivator cassettes, invertase cassettes and/or insertion cassettes. Furthermore, it may comprise a heterologous nucleic acid, in particular, the heterologous nucleic acids may be inserted into a gene expression cassette, thus rendering the GEC functional.

A still further aspect of the invention relates to the use of a nucleic acid molecule comprising at least 100 nucleotides of the nucleic acid sequence

shown in one of Figs.24A, B or hybridizing therewith and having promoter activity, for the in vivo inducible expression of a heterologous nucleic acid molecule.

- 5 A further aspect of the present invention is the use of said nucleic acid molecule for the detection of in vivo inducible promoters.

Experimental Procedures

- 10 The strains, material, and methods used in the type III secretion system of the *Salmonella* Pathogenicity Island 2 (SPI2) work described above are as follows:

Mice

15

Female BALB/c (H-2^d) of 6-12 weeks of age were maintained under standard conditions according to institutional guidelines. This study was approved by an ethic committee for animal use in experimental research.

- 20 *Bacterial strains, phages and plasmids*

The bacterial strains, phages and plasmids used in this study are listed in Table 1. Unless otherwise indicated, bacteria were grown at 37°C in Luria Bertani (LB) broth or agar, supplemented with ampicillin (50 µg/ml),
25 kanamycin (50 µg/ml), or chloramphenicol (50 µg/ml) where appropriate. Eukaryotic cells were grown in RPMI 1640 supplemented with 10% of

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foetal calf serum (FCS), 100 U/ml penicillin, 50 μ g/ml streptomycin, 5×10^{-5} M 2-mercaptoethanol and 1 mM L-glutamine (GIBCO BRL; Pringle, Scotland). To achieve constitutive expression of β -gal, the plasmid pAH97 (Holtel *et al.*, 1992) was electroporated into the carrier strains as described elsewhere (O'Callaghan and Charbit, 1990).

Table 1. Phages, plasmids and bacterial strains used in this work.

10	Phage, plasmid or strain	Description	Reference
	Phages		
	λ 1	clone from a library of <i>S. typhimurium</i> genomic DNA in λ 1059	Shea <i>et al.</i> , 1996
	λ 2	clone from a library of <i>S. typhimurium</i> genomic DNA in λ 1059	Shea <i>et al.</i> , 1996
15	λ 5	clone from a library of <i>S. typhimurium</i> genomic DNA in λ 1059	Shea <i>et al.</i> , 1996
	Plasmids		
	pBluescriptKS+	Amp ^r ; high copy number cloning vectors	Stratagene,
	pBluescriptSK+		Heidelberg
	pUC18	Amp ^r ; high copy number cloning vector	Gibco-BRL,
			Eggenstein
20	pT7-Blue	Amp ^r ; high copy number cloning vector	Novagen, Heidelberg

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	pCVD442	suicide vector	Donnenberg et al., 1991
	pACYC184	Cm ^r , Tet ^r ; low copy number cloning vector	Chang and Cohen, 1978
	pGPL01	R6K ori, Amp ^r ; λ pir-dependent suicide vector for <i>luc</i> fusions	Gunn and Miller, 1996
5	pLB02	R6K ori, Amp ^r ; λ pir-dependent suicide vector for <i>luc</i> fusions	Gunn and Miller, 1996
	pGP704	R6K ori, Amp ^r ; λ pir-dependent suicide vector	Miller and Mekalanos, 1988
	pKAS32	Amp ^r ; λ pir-dependent suicide vector; <i>rpsL</i> ^S	Skorupski and Taylor, 1996
	pNQ705	R6K ori, Cm ^r ; λ pir-dependent suicide vector	Forsberg et al., 1994
10	pSB315	Kan ^r , Amp ^r	Galán et al., 1992
	p1-6	Amp ^r , 4.8kb <i>Pst</i> I/ <i>Bam</i> HI fragment of λ 1 in pT7-Blue	this work
	p1-20	1.7kb <i>Bam</i> HI/ <i>Hinc</i> II fragment of p1-6 in pKS+	this work
	p1-21	<i>aphT</i> cassette in <i>Eco</i> RV site of p1-20	this work
	p1-22	<i>Xba</i> I/ <i>Kpn</i> I insert of p1-21 in pKAS32	this work
	p2-2	Amp ^r , 5.7kb <i>Bam</i> HI fragment of λ 2 in pUC18	this work
15	p2-20	1.6kb <i>Hind</i> III/ <i>Hinc</i> II fragment of p2-2 in <i>Hind</i> III/ <i>Sma</i> I-digested pKS+	this work
	p2-21	<i>aphT</i> cassette in <i>Hinc</i> II site of p2-20	this work
	p2-22	insert of p2-21 in pKAS32	this work
	p2-50	3.7kb <i>Bam</i> HI/ <i>Kpn</i> I fragment of p2-2 in pKS+	this work
	p5-2	Amp ^r ; 5.7kb <i>Eco</i> RI fragment of λ 5 in pKS+	this work
20	p5-30	3.0kb <i>Pst</i> I/ <i>Eco</i> RI fragment of p5-2 in pUC18	this work
	p5-31	<i>aphT</i> cassette in <i>Eco</i> RV site of p5-30	this work

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	p5-33	SphI/ <i>Eco</i> RI insert of p5-31 in pGP704	this work
	p5-4	Amp ^r ; 5.8kb <i>Hind</i> III fragment of λ 5 in pSK+	this work
	p5-40	4.5kb <i>Sst</i> I/ <i>Hind</i> III fragment of p5-2 in pKS+	this work
	p5-41	<i>aph</i> T cassette in <i>Sma</i> I site of p5-40	this work
5	p5-43	<i>Kpn</i> I/ <i>Sst</i> I insert of p5-41 in pNQ705	this work
	p5-5	Amp ^r ; <i>Pst</i> I digestion of p5-4 and religation of the larger fragment	this work
	p5-50	2.6kb <i>Bam</i> HI/ <i>Cl</i> aI fragment of p5-2 in pKS+	this work
	p5-51	<i>aph</i> T cassette in <i>Hind</i> III site of p5-50 after Klenow fill-in	this work
	p5-53	<i>Xba</i> I/ <i>Sal</i> I insert of p5-51 in pGP704	this work
10	p5-60	<i>Cl</i> aI-digestion of p5-2 and religation of larger fragment	this work
	p5-8	Amp ^r , 2.2kb <i>Pst</i> I/ <i>Hind</i> III fragment of p5-2 in pSK+	this work
	psseA	Cm ^r ; <i>sseA</i> in pACYC184	this study
	psseB	Cm ^r ; <i>sseB</i> in pACYC184	this study
	psseC	Cm ^r ; <i>sseC</i> in pACYC184	this work
15	<i>E. coli</i> strains		
	DH5 α	see reference	Gibco-BRL
	S17-1 λ pir	λ pir phage lysogen (see reference)	Miller and Mekalanos, 1988
	CC118 λ pir	λ pir phage lysogen (see reference)	Herrero <i>et al.</i> , 1990
20	XL1-Blue	see reference	Stratagene

S. typhimurium

strains

6	NCTC12023	wild-type	Colindale, UK
	CS015	<i>phoP</i> -102::Tn10d-Cm	Miller <i>et al.</i> , 1989
	CS022	<i>phoP^c</i>	Miller <i>et al.</i> , 1989
	P2D6	<i>ssaV</i> ::mTn5	Shea <i>et al.</i> , 1996
	P3F4	<i>ssrA</i> ::mTn5	Shea <i>et al.</i> , 1996
10	P4H2	<i>hilA</i> ::mTn5	Monack <i>et al.</i> , 1996
	P6E11	<i>spaRS</i> ::mTn5	Shea <i>et al.</i> , 1996
	P8G12	<i>ssrB</i> ::mTn5	Shea <i>et al.</i> , 1996
	P9B6	<i>ssaV</i> ::mTn5	Shea <i>et al.</i> , 1996
	P9B7	<i>ssaT</i> ::mTn5	Shea <i>et al.</i> , 1996
15	P11D10	<i>ssaJ</i> ::mTn5	Shea <i>et al.</i> , 1996
	NPssaV	<i>ssaV</i> :: <i>aphT</i> , Km ^r ; non-polar mutation	Deiwick <i>et al.</i> , 1998
	HH100	<i>sseA</i> Δ::: <i>aphT</i> , Km ^r ; non-polar mutation	this study
	HH101	HH100 containing <i>psseA</i>	this study
	HH102	<i>sseB</i> Δ::: <i>aphT</i> , Km ^r ; non-polar mutation	this study
20	HH103	HH102 containing <i>psseB</i>	this study
	HH107	<i>sseF</i> Δ::: <i>aphT</i> , Km ^r ; non-polar mutation	this study
	HH108	<i>sseG</i> :: <i>aphT</i> , Km ^r ; non-polar mutation	this study
	MvP102	Δ <i>sseEsscB</i> , Km ^r ; non-polar mutation	this work
	MvP103	<i>sseC</i> :: <i>aphT</i> , Km ^r ; non-polar mutation	this work
25	MvP103[<i>psseC</i>]	MvP103 containing <i>psseC</i>	this work
	MvP131	<i>ssaB</i> :: <i>luc</i> in <i>S. typhimurium</i> NCTC12023	this work
	MvP127	<i>sseA</i> :: <i>luc</i> in <i>S. typhimurium</i> NCTC12023	this work
	MvP239	<i>sipC</i> :: <i>lacZY</i> , EE638 in <i>S. typhimurium</i>	Hueck <i>et al.</i> , 1995;
		NCTC12023	this work
	MvP244	<i>ssaB</i> :: <i>luc</i> in <i>S. typhimurium</i> P8G12	this work

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	MvP266	<i>ssaH::luc</i> in <i>S. typhimurium</i> NCTC12023	this work
	MvP284	<i>ssrA::aphT</i> , Km ^r ; non-polar mutation	this work
	MvP320	<i>ssrB::aphT</i> , Km ^r ; non-polar mutation	this work
	MvP337	in-frame deletion in <i>sseC</i>	this work
5	MvP338	in-frame deletion in <i>sseD</i>	this work
	MvP339	in-frame deletion in <i>sscB</i>	this work
	MvP340	in-frame deletion in <i>ssrA</i>	this work
	SL7207	<i>S. typhimurium</i> 2337-65 <i>hisG46</i> ,	gift from
		DEL407 <i>aroA::TnI</i> (Tc-s)	B.A.D. Stocker
10	III-57 <i>sseC</i>	Δ <i>sseC</i>	this work

Example 1: Distribution of the pathogenicity island SPI-2 within different *Salmonella* strains

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The presence of open reading frames of the SPI-2 region in various *Salmonella* isolates and *E. coli* K-12 was analyzed by Southern hybridization as shown in Table 2.

20 Table 2: Prevalence of SPI-2 genes in various *Salmonella* ssp. deduced from representative gene probes

	Species	subspec.	serovar/serotype	<i>ssrAB</i>	ORF
	<i>S. enterica</i>	I	typhimurium	+	+
25	<i>S. enterica</i>	I	typhi	+	+
	<i>S. enterica</i>	II		+	+
	<i>S. enterica</i>	IIIa		+	+
	<i>S. enterica</i>	IIIb		+	+
	<i>S. enterica</i>	IV		+	+
30	<i>S. enterica</i>	VI		+	+
	<i>S. enterica</i>	VII		+	+
	<i>S. bongori</i>		66:z41:--	-	+
	<i>S. bongori</i>		44:z48:--	-	+
35	<i>E. coli</i> K-12			-	-

Presence or absence of hybridizing bands is indicated by + or -, respectively.

Hybridization

Genomic DNA of various *Salmonella* strains and *E. coli* K-12 was prepared as previously described (Hensel *et al.*, 1997a). For Southern hybridization analysis, genomic DNA was digested with *EcoRI* or *EcoRV*, fractionated on 0.6 % agarose gels and transferred to Hybond N⁺ membranes (Amersham, Braunschweig). Various probes corresponding to the SPI-2 region were obtained as restriction fragments of the subcloned insert of λ 1. Probes corresponding to ORF 242 and ORF 319 were generated by PCR using primer sets D89 (5'-TTTTTACGTGAAGCGGGGTG-3') and D90 (5'-GGCATTAGCGGATGTCTGACTG-3'), and D91 (5'-CACCAGGAACCATTTTCTCTGG-3') and D92 (5'-CAGCGATGACGATATTCGACAAG-3'), respectively. PCR was performed according to the specifications of the manufacturer (Perkin-Elmer, Weiterstadt). PCR products were submitted to agarose gel electrophoresis and fragments of the expected size were recovered and purified. Hybridization probes were labeled using the DIG labeling system as described by the manufacturer (Boehringer, Mannheim).

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Example 2: Characterization of *sse* genes and construction of *sseC::aphT*, *sseD::aphT* and *sseE* Δ mutant *S. typhimurium* strains MvP103, MvP101 and MvP102

25 Organization of *sse* and *ssc* genes

In order to characterize SPI2 genetically and functionally, a central region of the pathogenicity island (Fig. 1A) has been cloned and sequenced. DNA fragments covering the region between *ssaC* and *ssaJ* were subcloned in plasmids p5-2 and p5-4 as indicated in Fig. 1C. The arrangement and designation of genes in the 8kb region between *ssaC* and *ssaK* is shown in Fig. 1B. This sequence will be available from the EMBL database under

30

accession number AJ224892 in the near future. The sequenced region extends the open reading frame (ORF) of a gene encoding a putative subunit of the type III secretion apparatus referred to as *spiB* (Ochman *et al.*, 1996). For consistency with the universal nomenclature for type III secretion system subunits (Bogdanove *et al.*, 1996) and the nomenclature of other SPI2 genes (Hensel *et al.*, 1997b), this gene has been designated *ssaD*. The deduced amino acid sequence of *ssaD* is 24% identical to YscD of *Y. enterocolitica*. This is followed by an ORF with coding capacity for a 9.3 kDa protein, 34% identical to YscE of *Y. enterocolitica*. Therefore, this gene is designated *ssaE*. A sequence of 263 bp separates *ssaE* and a set of nine genes, several of which encode proteins with sequence similarity to secreted effector proteins or their chaperones from other pathogens. These genes are separated by short intergenic regions or have overlapping reading frames and it is likely that some are co-transcribed and translationally coupled. Therefore, the genes with similarity to those encoding chaperones were designated *sscA* and *sscB*, and the others *sseA-E*. The amino acid sequence deduced from *sscA* shows 26% identity/49% similarity over 158 amino acid residues to SycD, the product of *lcrH* of *Y. pseudotuberculosis* which acts as a secretion-specific chaperone for YopB and YopD (Wattiau *et al.*, 1994). The amino acid sequence deduced from *sscB* shows 23% identity/36% similarity over 98 amino acid residues to Ippl of *Shigella flexneri*. Ippl is a chaperone for *S. flexneri* invasion proteins (Ipas) (Baundry *et al.*, 1988). As is the case for the secretion chaperones SycD, Ippl and SicA (Kaniga *et al.*, 1995), SscB has an acidic pI (Table 3), whereas SscA has an unusually high pI of 8.8. SseB is 25% identical/47% similar to EspA of EPEC over the entire length of the 192 amino acid residue protein (Fig. 2b). SseD is 27% identical/51% similar to EspB of EPEC over 166 amino acid residues. SseC has sequence similarity to a class of effector proteins involved in the translocation of other effectors into the target host cell. These include YopB of *Y. enterocolitica*, EspD of EPEC and PepB of *Pseudomonas aeruginosa*. SseC is approximately 24% identical/48% similar to both EspD of EPEC and YopB of *Y. enterocolitica* (Fig. 2a). EspD

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and YopB have two hydrophobic domains that are predicted to insert into target cell membranes (Pallen *et al.*, 1997). SseC contains three hydrophobic regions that could represent membrane-spanning domains. Other features of these predicted effector proteins are shown in Table 1.

5 Using the TMpredict program (Hofmann and Stoffel, 1993), transmembrane helices are predicted for all the effector proteins apart from SseA which is very hydrophilic. Alignments of SseC to homologs in other pathogens are shown in Fig. 2b. Conserved amino acids are mainly clustered in the central, more hydrophobic portion of the protein, but unlike YopB, there is

10 no significant similarity to the RTX family of toxins. The conserved residues in SseD are present mainly in the N-terminal half of the protein. Comparison of the deduced amino acid sequences of *sseABCDEF* with entries in the PROSITE database did not reveal the presence of any characteristic protein motifs. We subjected the predicted amino acid sequences of the *sse* genes

15 to searches using the programs COIL and MULTICOIL as described by Pallen *et al.* (1997). SseA and SseD are predicted to have one trimeric coil each, and SseC is predicted to have two trimeric coils (Table 3). Since EspB and EspD are predicted to have one and two trimeric coils, respectively (Pallen *et al.*, 1997), this provides further evidence that these proteins are

20 functionally related.

Table 3. Features of predicted proteins.

25	Protein	M _r (kDa)	pI	Tm predictions	Predicted coils
	SseA	12.5	9.3	hydrophilic	at least one (trimer)
	SseB	21.5	4.7	one transmembrane helix	none
	SseC	52.8	6.3	three transmembrane helices	at least two (trimers)
	SseD	20.6	4.8	three transmembrane helices	at least one (trimer)
30	SseE	16.3	9.7	one transmembrane helix	none
	SscA	18.1	8.8	hydrophilic	none
	SscB	16.4	4.7	hydrophilic	none

Expression of SPI2 genes

Generation of antibodies against recombinant SPI2 proteins

- 5 In order to monitor the expression of the SPI2 genes *sseB*, *sscA* and *ssaP*, a Western blot analysis of total bacterial cells with polyclonal antibodies raised against recombinant SPI2 proteins SseB, SscA, and SsaP was performed.
- 10 Protein gel electrophoresis and Western blotting were performed as described elsewhere (Laemmli, 1970 and Sambrook *et al.*, 1989). Plasmids for the expression of recombinant SPI2 protein were constructed by cloning the individual SPI2 genes in plasmids pQE30, pQE31 or pQE32 (Qiagen, Hilden) in order to generate in-frame fusion to the N-terminal 6His tag.
- 15 Recombinant SPI2 genes were expressed in *E. coli* M15 [pREP] (Qiagen) and purified by metal chelating chromatography according to recommendations of the manufacturer (Qiagen). For immunisation, about 1 mg of recombinant SPI2 proteins were emulsified with complete and incomplete Freund's adjuvant for primary and booster immunizations, respectively. Rabbits were
- 20 immunized subcutaneously according to standard protocols (Harlow and Lane, 1988). SPI2 proteins were detected with antisera raised against recombinant SPI2 proteins after electrophoretical separation of proteins from total cells and transferred onto a nitrocellulose membrane (Schleicher and Schuell) using a 'Semi-Dry' blotting device (Bio-Rad) according to the
- 25 manufacturers manual. Bound antibody was visualized using a secondary antibody-alkaline phosphatase conjugate according to standard protocols (Harlow and Lane).

Generation of reporter gene fusions:

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Fusions of the reporter gene firefly luciferase (*luc*) to various genes in SPI2 were obtained using the suicide vectors pLB02 and pGPL01 (Gunn and

Miller, 1996), which were kindly provided by Drs. Gunn and Miller (Seattle).

For the generation of a fusion to *ssaB*, a 831 bp *EcoRV* fragment of p2-2
5 was subcloned in *EcoRV* digested pSK⁺. For the generation of a
transcriptional fusion to *sseA*, a 1060 bp *SmaI/HincII* fragment of p5-4 was
subcloned in pSK⁺. The inserts of the resulting constructs were recovered
as a *EcoRI/KpnI* fragment and ligated with *EcoRI/KpnI* digested reporter
vectors pGPL01 and pLB02. For the generation of a transcriptional fusion
10 to *ssaJ*, a 3kb *SmaI/KpnI* fragment of p5-2 was directly subcloned in
pGPL01 and pLB02.

Constructs with transcriptional fusions of SPI2 genes to *luc* were then
integrated into the chromosome of *S. typhimurium* by mating between *E.*
15 *coli* S17-1 λ pir harbouring the respective construct and a spontaneous
mutant of *S. typhimurium* resistant to 100 μ g x ml⁻¹ nalidixic acid and
selection for exconjugants resistant to carbenicillin and nalidixic acid. The
targeted integration in SPI2 (for constructs using pGPL01) or the *zch* region
(for constructs using pLB02) was confirmed by Southernanalysis. Fusions
20 were then moved into a mouse-passaged strain of *S. typhimurium*
NCTC12023 by P22 transduction according to standard procedures (Maloy
et al., 1996).

Assay of reporter genes

25 β -galactosidase activities of reporter gene fusions were determined
according to standard procedures (Miller, 1992).

Bacterial strains harbouring firefly luciferase fusions to SPI2 genes (strain
MvP127, *sseA::luc*, strain MvP131, *ssaB::luc*, strain MvP266, *ssaH::luc*)
30 were grown in medium with various Mg²⁺ concentrations. The luciferase
activity of aliquots of the cultures was determined using the Promega
(Heidelberg) luciferase assay kit or custom made reagents accordingly.

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Briefly, bacteria were pelleted by centrifugation for 5 min. at 20000 x g at 4°C and resuspended in lysis buffer (100 mM KHPO₄, pH 7.8, 2 mM EDTA, 1 % Triton X-100, 5 mg x ml⁻¹ bovine serum albumin, 1 mM DTT, 5 mg x ml⁻¹ lysozyme). Lysates were incubated for 15 min at room temperature with repeated agitation and subjected to a freeze/thaw cycle. Aliquots of the lysates (25 µl) were transferred to microtiter plates (MicroFLUOR, Dynatech) and immediately assayed after addition of 50 µl luciferase reagent (20 mM Tricine-HCl, pH 7.8, 1.07 mM (MgCO₃)₄Mg(OH)₂, 100 µM EDTA, 33.3 mM DTT, 270 µM Li₃-coenzyme A, 470 µM D(-)-luciferin, 530 µM Mg-ATP) for photon emission using the TriLux MicroBeta luminometer (Wallac, Turku). All assays were done in triplicates and repeated on independent occasions.

Expression of SPI2 genes such as ssaB and ssaH is induced by low Mg²⁺ concentrations of the growth medium

S. typhimurium wild-type strain and strains harbouring luc reporter-gene fusions to *ssaB* (strain MvP131) and to *ssaH* (strain MvP266) were grown to mid-log phase (OD at 600 nm of about 0.5) in minimal media containing high amounts of Mg²⁺ (10 mM MgCl₂). This medium is referred to as medium G. Bacteria were recovered by centrifugation, washed three times in minimal medium containing 8 µM Mg²⁺. This medium is referred to as medium F. Bacteria were resuspended in medium F or medium G and growth at 37°C was continued. Aliquots of the cultures of strains MvP131 and MvP266 were withdrawn at the several different time points indicated and subjected to analysis of luciferase activity. Aliquots of the wild-type strain were withdrawn at the same time points. Protein from total bacterial cells was separated by SDS-PAGE and transferred to nitrocellulose membranes. These blots were incubated with antibodies raised against recombinant SsaP and SsaA protein in order to detect proteins synthesized after the magnesium concentration shift in the magnesium concentration.

After shifting bacteria from a growth medium with high amounts of Mg^{2+} to a medium with limiting amounts of Mg^{2+} , the expression of SPI2 genes was highly induced. This induction can be monitored by using the reporter gene *luc* fused into different positions of SPI2. Furthermore, proteins synthesized after induction of SPI2 were detected by Western Blots. However, even in the presence of high amounts of Mg^{2+} , a low level of expression of SPI2 genes was observed.

Expression of SPI2 genes such as sseA and ssaB is modulated by PhoP/PhoQ regulation

No expression of *sseB* or *sscA* was observed during growth in various rich media, or cell culture media with or without serum. However, low amount of SsaP were detected after growth in LB or other rich media such as brain heart infusion (BHI). Growth in minimal medium containing less than $30 \mu M$ Mg^{2+} induces the expression of SPI2 genes. Such effect of the Mg^{2+} concentration has so far only been observed for PhoP/PhoQ-regulated genes. This observation is in contrast to a previous report by Valdivia and Falkow (1997) who postulated that SPI2 gene expression is independent of PhoP/PhoQ. However, in a $PhoP^c$ (constitutive) strain background (CS022, Miller *et al.*, 1989) expression of SPI2 genes was not constitutive but still dependent on the Mg^{2+} concentration of the medium. This indicates that SPI2 gene expression is modulated by PhoP/PhoQ, but that further regulatory elements such as SsrA/B are needed.

DNA cloning and sequencing

DNA preparations and genetic manipulations were carried out according to standard protocols (Sambrook *et al.*, 1989). Plasmid DNA transformation of bacterial cells was performed by electroporation (O'Callaghan and Charbit, 1990).

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Clones harbouring fragments of SPI2 were identified from a library of genomic DNA of *S. typhimurium* in λ 1059 which has been described previously (Shea *et al.*, 1996). The *sse* and *ssc* genes were subcloned from clone λ 5 on a 5.7kb *EcoRI* fragment (p5-2) and a 5.8kb *HindIII* fragment (p5-4) in pBluescriptKS+ as indicated in Fig. 1 and Table 1.

DNA sequencing was performed using a primer-walking strategy. The dideoxy method (Sanger *et al.*, 1977) was applied using the Pharmacia T7 sequencing system for manual sequencing and the dye terminator chemistry for automatic analysis on a ABI377 sequencing instrument. Assembly of contigs from DNA sequences was performed by means of AssemblyLign and MacVector software (Oxford Molecular, Oxford). For further sequence analyses, programs of the GCG package version 8 (Devereux *et al.*, 1984) were used on the HGMP network.

Construction of non-polar mutations

The construction of non-polar mutations in *sseC* (MvP103), *sseD* (MvP101) and *sseE* (MvP102) are described below. All chromosomal modifications were confirmed by PCR and Southern hybridization analysis (Southern, 1975, J. Mol. Biol. 98: 503-517).

- Mutant MvP103, *sseC*. A 2.6kb fragment was recovered after *Bam*HI and *Cla*I digestion of p5-2 and subcloned in *Bam*HI/*Cla*I-digested pBluescript II KS+. The resulting construct termed p5-50 was digested by *Hind*III, blunt ended using the Klenow fragment of DNA polymerase and ligated to the *aphT* cassette. A 900 bp *Hinc*II fragment of pSB315 containing an aminoglycoside 3'-phosphotransferase gene (*aphT*) from which the transcriptional terminator had been removed (Galán *et al.*, 1992) was ligated in the

same orientation into the blunted-ended *Hind*III site of plasmid p5-50. After transformation of *E. coli* XL-1 Blue and selection for resistance against kanamycin and carbenicillin (50 µg/ml each) one clone has been chosen and the harbouring plasmid isolated. This plasmid was termed p5-51 and its identity confirmed by restriction analysis. It was further digested with *Sal*I and *Xba*I and the insert of 3.5kb was ligated to *Sal*I/*Xba*I-digested pGP704. This plasmid was electroporated into *E. coli* CC118 λ pir and the transformants selected for resistance to kanamycin and carbenicillin (50 µg/ml each). As done before, one clone was chosen, its plasmid with the according DNA fragment in pGP704, termed p5-53, isolated and confirmed by restriction analysis. Plasmid p5-53 was electroporated into *E. coli* S17-1 λ pir and transferred into *S. typhimurium* NCTC12023 (resistant to nalidixic acid, 100 µg/ml) by conjugation as has been described previously (de Lorenzo and Timmis, 1994). Exconjugants in which the *sseC* gene had been replaced by the cloned gene disrupted by insertion of the *aphT* cassette were selected by resistance to kanamycin and nalidixic acid (100 µg/ml). The resulting exconjugants were finally tested for a lactose-negative phenotype and their sensitivity to carbenicillin. Selected clones were further examined by Southernblot analysis. In order to exclude possible mutations which have been acquired during the cloning procedure the mutated *sseC* allele was transferred into a fresh *Salmonella* background by P22 transduction (described by Maloy *et al.*, 1996). The resulting *Salmonella* strain MvP103 was examined for the presence of the resistance cassette within the *sseC* gene by the use of PCR. Amplification was performed by using the primers E25 (5'-GAAATCCCGCAGAAATG-3') and E28 (5'-AAGGCGATAATATAAAC-3'). The resulting fragment had a size of 1.6kb for *S. typhimurium* wild-type and 2.5kb for strain MvP103.

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For complementation of non-polar mutations in *sseC*, the corresponding genes were amplified by PCR from genomic DNA using a series of primers corresponding to the region 5' of the putative start codons and to the 3' ends of the genes. These primers introduced *Bam*HI restriction sites at the termini of the amplified genes. After digestion with *Bam*HI, the genes were ligated to *Bam*HI-digested pACYC184 (Chang and Cohen, 1978) and transferred into *E. coli* DH5 α . The orientation of the insert was determined by PCR, and in addition, DNA sequencing was performed to confirm the orientation and the correct DNA sequence of the inserts. Plasmids with inserts in the same transcriptional orientation as the Tet^r gene of pACYC184 were selected for complementation studies and electroporated into the *S. typhimurium* strains harbouring corresponding non-polar mutations.

- Mutant MvP101, *sseD*. A 3.0kb fragment was recovered after *Pst*I and *Eco*RI digestion of p5-2 and subcloned in *Pst*I/*Eco*RI-digested pUC18. The resulting construct termed p5-30 was digested by *Eco*RV and treated with alkaline phosphatase. The *aph*T cassette was isolated as described above and ligated to the linearized plasmid p5-30 in the same orientation in the unique *Eco*RV site. After transformation of *E. coli* XL-1 Blue and selection against kanamycin and carbenicillin (50 μ g/ml each) one clone has been chosen and the harbouring plasmid isolated. This plasmid was termed p5-31 and its identity confirmed by restriction analysis. p5-31 was further digested with *Sph*I and *Eco*RI, a 4.0kb fragment isolated and ligated to *Sph*I/*Eco*RI-digested pGP704. This plasmid was electroporated into *E. coli* CC118 λ pir and transformants selected to kanamycin and carbenicillin (50 μ g/ml each). As done before, one clone was chosen, its plasmid with the according DNA fragment in pGP704, termed p5-33, isolated and confirmed by restriction analysis. Plasmid p5-33 was electroporated into *E. coli* S17-1 λ pir and transferred into *S.*

typhimurium NCTC12023 (resistant to nalidixic acid) by conjugation as has been described previously (de Lorenzo and Timmis, 1994). Exconjugants in which the *sseD* gene had been replaced by the cloned gene disrupted by insertion of the *aphT* cassette were selected by resistance to kanamycin and nalidixic acid (100 µg/ml). The resulting exconjugants were finally tested for a lactose-negative phenotype and their sensitivity to carbenicillin. Selected clones were further examined by Southernblot analysis. In order to exclude possible mutations which might have been accumulated during the cloning procedure the mutated *sseD* allele was transferred into a fresh *Salmonella* background by P22 transduction (described by Maloy *et al.*, 1996). The resulting *Salmonella* strain MvP101 was examined for the presence of the resistance cassette within the *sseD* gene by the use of PCR. Amplification was performed by using the primers E6 (5'-AGAGATGTATTAGATAC-3') and E28 (5'-AAGGCGATAATATAAAC-3'). The resulting fragment had a size of 0.8kb for *S. typhimurium* wild-type, was used and 1.7kb in the case of strain MvP101.

Mutant MvP102, deletion of parts of *sseE* and *sscB*. A 4.5kb fragment was recovered after *SstI* and *HindIII* digestion of p5-2 and subcloned in *SstI/HindIII*-digested pKS+. The resulting construct termed p5-40 was digested by *SmaI*, digested with alkaline phosphatase and ligated to the *aphT* cassette in the same orientation into the unique *SmaI* site created in the *sseE/sseB* deletion plasmid p5-40 as described above. After transformation of *E. coli* XL-1 Blue and selection against kanamycin and carbenicillin (50 µg/ml each) one clone was chosen and the harbouring plasmid isolated. This plasmid was termed p5-41 and its identity confirmed via restriction analysis. It was further digested with *KpnI* and *SstI* and the insert was ligated

to *KpnI/SstI*-digested pNQ705. This plasmid was electroporated into *E. coli* CC118 λ pir and transformed bacteria selected to kanamycin and chloramphenicol (50 μ g/ml each). As done before, one clone was chosen, its plasmid with the according DNA fragment in pNQ705, termed p5-43, isolated and confirmed by restriction analysis. The resulting plasmid was used to transfer the mutated gene onto the *Salmonella* chromosome as described above. Resulting clones have been further examined by Southernblot analysis. To exclude possible mutations which might have been acquired during the cloning procedure the mutated *sseE/sscB* allele was transferred into a fresh *Salmonella* background by P22 transduction (described by Maloy *et al.*, 1996). The resulting *Salmonella* strain MvP102 was examined for the presence of the resistance cassette within the *sseE/sseB* gene by the use of PCR. Amplification was performed by using the primers E6 (5' - AGAGATGTATTAGATAC - 3') and E4 (5' - GCAATAAGAGTATCAAC - 3'). The resulting fragment had a size of 1.6kb for *S. typhimurium* wild-type and a size of 1.9kb for strain MvP102.

20 Construction of mutant strains carrying in-frame deletions in *sseC*, *sseD* and *sscB*:

Based on the observation that a non-polar in *sseE* did not result in a significant attenuation of virulence in the mouse model (Hensel *et al.*, 1998), the generation of a deletion mutant for the *sseE* gene is not of interest for the generation of carrier strains.

Construction of an in-frame deletion in *sseC*, mutant MvP337

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A deletion of 158 bp between codon 264 and 422 of *sseC* was generated. Plasmid p5-2 was digested by *Cla*I and the larger fragment containing the vector portion was recovered and self-ligated to generate p5-60. Plasmid p5-60 was linearized by digestion with *Hind*III, which cuts once within the *sseC* gene. Primers *sseC*-del-1 (5'- GCT AAG CTT CGG CTC AAA TTG TTT GGA AAA C -3') and *sseE*-del-2 (5'- GCT AAG CTT AGA GAT GTA TTA GAT ACC -3') were designed to introduce *Hind*III sites. PCR was performed using linearized p5-60 as template DNA. The TaqPlus polymerase (Stratagene) was used according to the instructions of the manufacturer. Reactions of 100 μ l volume were set up using 10 μ l of 10 x TaqPlus Precision buffer containing magnesium chloride, 0.8 μ l of 100 mM dNTPs, 250 ng DNA template (linearized p5-8), 250 ng of each primer and 5 U of TaqPlus DNA polymerase. PCR was carried out for 35 cycles of: 95°C for 1 minute, 60°C for 1 minute, 72°C for 6 minutes. Then a final step of 72°C for 10 minutes was added. 10 μ l of the PCR reaction were analyzed. A product of the expected size was recovered, digested by *Hind*III, self-ligated, and the ligation mixture was used to transform *E. coli* DH5 α to resistance to carbenicillin. Plasmids were isolated from transformants and the integrity of the insert and the deletion was analyzed by restriction digestion and DNA sequencing. The insert of a confirmed construct was isolated after digestion with *Xba*I and *Kpn*I and ligated to *Xba*I/*Kpn*I-digested vector pKAS32. The resulting construct was used to transform *E. coli* S17-1 Δ pir to resistance to carbenicillin, and conjugational transfer of the plasmid to *S. typhimurium* (Nal^R, Strep^R) was performed according to standard procedures (de Lorenzo and Timmis, 1994). Exconjugants that had integrated the suicide plasmid by homologous recombination were selected by resistance to nalidixic acid and carbenicillin, and screened for sensitivity to streptomycin. Such clones were grown in LB to OD600 of about 0.5 and aliquots were plated on LB containing 250 μ g/ml streptomycin to select for colonies which had lost the integrated plasmid and undergone allelic

exchange. Clones resistant to streptomycin but sensitive to carbenicillin were used for further analysis. Screening of mutants with a deletion within the *sseC* locus was performed by PCR using primers *sseC*-For (5'- ATT GGA TCC GCA AGC GTC CAG AA -3') and *sseC*-Rev (5- TAT GGA TCC TCA GAT TAA GCG CG-3'). Amplification of DNA from clones containing the wild-type *sseC* allele resulted in a PCR product of 1520 bp, use of DNA from clones harbouring a *sseC* allele with an internal deletion resulted in a PCR product of 1050 bp. The integrity of clones harbouring the *sseC* deletion was further confirmed by Southern analysis of the *sseC* locus. Finally, the *sseC* locus containing the internal in-frame deletion was moved into a fresh strain background of *S. typhimurium* by P22 transduction (Maloy *et al.*, 1996) and the resulting strain was designated MvP 337.

Construction of an in-frame deletion in sseD, mutant strain MvP338

A deletion of 116 bp between codon 26 and 142 of *sseD* was generated. Plasmid p5-2 was digested by *HindIII*/*PstI* and a fragment of 2.1kb was isolated and subcloned in *HindIII*/*PstI*-digested vector pBluescript SK+. The resulting construct was designated p5-8. p5-8 was linearized by digestion with *EcoRV*, which cuts twice within the *sseD* gene. Primers *sseD*-del-1 (5'- ATA GAA TTC GGA GGG AGA TGG AGT GGA AG -3') and *sseD*-del-2 (5'- ATA GAA TTC GAA GAT AAA GCG ATT GCC GAC -3') were designed to introduce *EcoRI* sites. PCR was performed using linearized p5-8 as template DNA. The TaqPlus polymerase (Stratagene) was used according to the instructions of the manufacturer. Reactions of 100 µl volume were set up using 10 µl of 10 x TaqPlus Precision buffer containing magnesium chloride, 0.8 µl of 100 mM dNTPs, 250 ng DNA template (linearized p5-8), 250 ng of each primer and 5 U of TaqPlus DNA polymerase. PCR was carried out for 35 cycles of: 95°C for 1 minute, 60°C for 1 minute, 72°C for 5 minutes. Then a final step of 72°C for 10 minutes was added. 10 µl of the

PCR reaction were analyzed. A product of the expected size was recovered, digested by *EcoRI*, self-ligated, and the ligation mixture was used to transform *E. coli* DH5 α to resistance to carbenicillin. Plasmids were isolated from transformants and the integrity of the insert and the deletion was analyzed by restriction mapping and DNA sequencing. The insert of a confirmed construct was isolated after digestion with *XbaI* and *KpnI* and ligated to *XbaI/KpnI*-digested vector pKAS32. The resulting construct was used to transform *E. coli* S17-1 λ pir to resistance to carbenicillin, and conjugational transfer of the plasmid to *S. typhimurium* (Nal^R, Strep^R) was performed according to standard procedures (de Lorenzo and Timmis, 1994). Exconjugants that had integrated the suicide plasmid by homologous recombination were selected by resistance to nalidixic acid and carbenicillin, and screened for sensitivity to streptomycin. Such clones were grown in LB to OD600 of about 0.5 and aliquots were plated on LB containing 250 μ g/ml streptomycin to select for colonies which had lost the integrated plasmid and undergone allelic exchange. Clones resistant to streptomycin but sensitive to carbenicillin were used for further analysis. Screening of mutants with a deletion within the *sseD* locus was performed by PCR using primers *sseD*-For (5'- GAA GGA TCC ACT CCA TCT CCC TC -3') and *sseD*-Rev (5'- GAA GGA TCC ATT TGC TCT ATT TCT TGC -3'). Amplification of DNA from clones containing the wild-type *sseD* allele resulted in a PCR product of 560 bp, use of DNA from clones harbouring a *sseD* allele with an internal deletion resulted in a PCR product of 220 bp. The integrity of clones harbouring the *sseD* deletion was further confirmed by Southernanalysis of the *sseD* locus. Finally, the *sseD* locus containing the internal in-frame deletion was moved into a fresh strain background of *S. typhimurium* by P22 transduction (Maloy *et al.*, 1996) and the resulting strain was designated MvP338.

Construction of an in-frame deletion in *sscB*, mutant strain MvP339

A deletion of 128 bp between codon 32 and 160 of *sscB* was generated. A 3kb *Bgl*II fragment of plasmid p5-2 was ligated into the *Bam*HI site of pBluescript KS+ to generate plasmid p5-70. Plasmid p5-70 was linearized
5 by digestion with *Nco*I, which cuts once within the *sscB* gene. Primers *sscB*-del-1 (5'- ATG GGA TCC GAG ATT CGC CAG AAT GCG CAA -3') and *sscB*-del-2 (5'- ATG GGA TCC ACT GGC ATA AAC GGT TTC CGG -3') were designed to introduce *Bam*HI sites. PCR was performed using linearized p5-70 as template DNA. The TaqPlus polymerase (Stratagene)
10 was used according to the instructions of the manufacturer. Reactions of 100 μ l volume were set up using 10 μ l of 10 x TaqPlus Precision buffer containing magnesium chloride, 0.8 μ l of 100 mM dNTPs, 250 ng DNA template (linearized p5-70), 250 ng of each primer and 5 U of TaqPlus DNA polymerase. PCR was carried out for 35 cycles of: 95°C for 1 minute,
15 60°C for 1 minute, 72°C for 6 minutes. Then a final step of 72°C for 10 minutes was added. 10 μ l of the PCR reaction were analyzed. A product of the expected size was recovered, digested by *Bam*HI, self-ligated, and the ligation mixture was used to transform *E. coli* DH5 α to resistance to carbenicillin. Plasmids were isolated from transformants and the integrity of
20 the insert and the deletion was analyzed by restriction analysis and DNA sequencing. The insert of a confirmed construct was isolated after digestion with *Xba*I and *Kpn*I and ligated to *Xba*I/*Kpn*I-digested vector pKAS32. The resulting construct was used to transform *E. coli* S17-1 λ pir to resistance to carbenicillin, and conjugational transfer of the plasmid to *S. typhimurium*
25 (Nal^R, Strep^R) was performed according to standard procedures (de Lorenzo and Timmis, 1994). Exconjugants that had integrated the suicide plasmid by homologous recombination were selected by resistance to nalidixic acid and carbenicillin, and screened for sensitivity to streptomycin. Such clones were grown in LB to OD600 of about 0.5 and aliquots were plated on LB
30 containing 250 μ g/ml streptomycin to select for colonies which had lost the

integrated plasmid and undergone allelic exchange. Clones resistant to streptomycin but sensitive to carbenicillin were used for further analysis. Screening of mutants with a deletion within the *sseC* locus was performed by PCR using primers *sscB*-For (5'- ATT GGA TCC TGA CGT AAA TCA TTA TCA -3') and *sscB*-Rev (5- ATT GGA TCC TTA AGC AAT AAG TGA ATC -3'). Amplification of DNA from clones containing the wild-type *sscB* allele resulted in a PCR product of 480 bp, use of DNA from clones harbouring a *sscB* allele with an internal deletion resulted in a PCR product of 100 bp. The integrity of clones harbouring the *sseC* deletion was further confirmed by Southernanalysis of the *sscB* locus. Finally, the *sscB* locus containing the internal in-frame deletion was moved into a fresh strain background of *S. typhimurium* by P22 transduction (Maloy *et al.*, 1996) and the resulting strain was designated MvP339.

15 Construction of a deletion mutation in the *sseC* gene

In a further approach the complete sequence of the chromosomal *sseC* gene was deleted by allelic replacement with a deleted copy of the gene. The deletion was constructed in a suicide plasmid (pCVD442 (Donnenberg *et al.*, 1991). First, two DNA fragments flanking the *sseC* gene (fragment A, carrying artificial *SaII* and *XbaI* sites at its 5' and 3' ends, respectively; and fragment B, carrying artificial *XbaI* and *SacI* sites at its 5' and 3' ends, respectively) were amplified by PCR. The oligonucleotides used for PCR were: 1.) *sseDelfor1* GCTGTGCGACTTGTAGTGAGTGAGCAAG (3' nucleotide corresponds to bp 941 in included sequence: Fig 21A); 2.) *sseCDelrev2* GGATCTAGATTTTAGCTCCTGTCAGAAAG (3' nucleotide corresponds to bp 2585 in included sequence, oligo binds to reverse strand); 3.) *sseCDelfor2* GGATCTAGATCTGAGGATAAAAATATGG (3' nucleotide corresponds to bp 4078 in included sequence); 4.) *sseDelrev1* GCTGAGCTCTGCCGCTGACGGAATATG (3' nucleotide corresponds to bp

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5592 in included sequence, oligo binds to reverse strand). The resulting PCR fragments were fused together via the *Xba*I site. The resulting fragment was cut with *Sall* and *Sac*I and cloned into pCVD442 cut with *Sall* and *Sac*I. The resulting plasmid was introduced into *S.typhimurium* NCTC12023 by conjugation and chromosomal integrants of the plasmid into the *sseC* locus were selected for by the plasmid-encoded ampicillin resistance marker. In a second step, clones which had lost the plasmid were screened for by loss of ampicillin resistance. The resulting clones were tested for chromosomal deletion of the *sseC* gene by PCR, and deletion of a 1455 bp fragment, comprising the entire *sseC* open reading frame, was confirmed. This Δ *sseC* mutant strain was named III-57 Δ *sseC*.

Construction of a *sseC-aroA* double mutant

15 In order to construct a double mutant which can serve as a prototype for a live attenuated vaccine, the *sseC:aphT* (Km^r) marker from MvP103 was transferred by P22 phage transduction into *S.typhimurium* SL7207 (*hisG46* DEL407 [*aroA544:Tn10*], Tc^R) a strain carrying a stable deletion in the *aroA* gene.

20

Example 3: Invasion and intracellular growth in tissue culture

Intramacrophage replication of mutant strains

25 Several strains which are defective in their ability to replicate inside macrophages and macrophage-like cell lines have been tested, as macrophage survival and replication are thought to represent an important aspect of *Salmonella* pathogenesis *in vivo* (Fields *et al.*, 1986). It has been reported previously that a number of SPI2 mutant strains were not defective
30 for survival or replication within RAW macrophages (Hensel *et al.*, 1997b)

but subsequent experiments have revealed that some SPI2 mutants can be shown to have a replication defect if aerated stationary phase bacterial cultures opsonized with normal mouse serum are used (see also accompanying paper: Cirillo *et al.*, 1998). The increase in cfu for different strains in RAW macrophages over a 16 h period is shown in Fig. 3. Replication defects were observed for strains carrying mutations in *ssaV* (encoding a component of the secretion apparatus), *sseB* and *sseC* and to a lesser extent for strains carrying mutations in *sseE*. Partial complementation of this defect was achieved with strains harbouring plasmids carrying functional copies of *sseB* and *sseC*, HH103 and MvP103[*psseC*], respectively. The ability of SPI2 mutant strains to replicate inside the J774.1 macrophage cell line (Fig. 4A) and in periodate-elicited peritoneal macrophages from C3H/HeN mice (Fig. 4B) has also been tested. Similar replication defects of *S. typhimurium* carrying transposon or non-polar mutations in SPI2 genes were observed, regardless of the phagocyte cell-type examined, although the peritoneal elicited cells had superior antimicrobial activity compared to either cell line.

20 *Macrophage survival assays*

RAW 264.7 cells (ECACC 91062702), a murine macrophage-like cell line, were grown in Dulbecco's modified Eagle's medium (DMEM) containing 10% foetal calf serum (FCS) and 2 mM glutamine at 37°C in 5% CO₂. *S. typhimurium* strains were grown in LB to stationary phase and diluted to an OD₆₀₀ of 0.1 and opsonized for 20 min in DMEM containing 10% normal mouse serum. Bacteria were then centrifuged onto macrophages seeded in 24 well tissue culture plates at a multiplicity of infection of approximately 1:10 and incubated for 30 min. Following infection, the macrophages were washed twice with PBS to remove extracellular bacteria and incubated for

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90 min (2h post-infection) or 16 h in medium containing gentamicin (12 μ g/ml). Infected macrophages were washed twice with PBS and lysed with 1% Triton X-100 for 10 min and appropriate aliquots and dilutions were plated onto LB agar to enumerate cfu.

5

Survival of opsonized *S. typhimurium* strains in J774.1 cells (Ralph *et al.*, 1975) or C3H/HeN murine peritoneal exudate cells (from Charles River Laboratories, Wilmington, MA) was determined essentially as described by DeGroote *et al.* (1997), but without the addition of interferon- γ . Briefly, peritoneal cells harvested in PBS with heat-inactivated 10% foetal calf serum 4 days after intraperitoneal injection of 5 mM sodium periodate (Sigma, St. Louis, MO) were plated in 96-well flat-bottomed microtiter plates (Becton-Dickinson, Franklin Lakes, NJ) and allowed to adhere for 2 h. Non-adherent cells were flushed out with prewarmed medium containing 10% heat-inactivated foetal calf serum. In previous studies, we have established that >95% of the cells remaining after this procedure are macrophages. *S. typhimurium* from aerated overnight cultures was opsonized with normal mouse serum and centrifuged onto adherent cells at an effector to target ratio of 1:10. The bacteria were allowed to internalize for 15 min, and washed with medium containing 6 μ g/ml gentamicin to kill extracellular bacteria. At 0 h and 20 h, cells were lysed with PBS containing 0.5% deoxycholate (Sigma, St. Louis, MO), with plating of serial dilutions to enumerate colony-forming units.

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Example 4: Evaluation of safety in the *S. typhimurium* mouse model of salmonellosis

Virulence tests with strains carrying non-polar mutations

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DNA sequence analysis suggested that the *sse* genes might encode effector proteins of the secretion system, but apart from a possible polar effect from a transposon insertion in *sscA* no strains carrying mutations in these genes were recovered in the original STM screen for *S. typhimurium* virulence genes using mTn5 mutagenesis (Hensel *et al.*, 1995), and their role in virulence was unclear. To address this question, strains carrying non-polar mutations in *sseC*, *sseD* and *sseEsscB* (Fig. 1) have been constructed and subjected to virulence tests. Table 4 shows that all mice inoculated with strains carrying mutations *sseC* and *sseD* survived a dose of 1×10^4 cfu, three orders of magnitude greater than the LD₅₀ of the wild-type strain, which is less than 10 cfu when the inoculum is administered by the i.p. route (Buchmeier *et al.*, 1993; Shea *et al.*, 1996). The same strains containing a plasmid carrying the corresponding wild-type allele were also inoculated into mice at a dose of 1×10^4 cfu. No mice survived these infections, which shows that each mutation can be complemented by the presence of a functional copy of each gene, and that each of these genes plays an important role in *Salmonella* virulence. Strains carrying non-polar mutations in *sseEsscB* caused lethal infections when approximately 1×10^4 cells of each strain were inoculated into mice by the i.p. route (Table 4) and were analyzed in more detail by a competition assay with the wild-type strain in mixed infections (five mice/test) to determine if they were attenuated in virulence. The competitive index, defined as the output ratio of mutant to wild-type bacteria, divided by the input ratio of mutant to wild-type bacteria, shows that the *sseEsscB* mutant was not significantly different to that of a fully virulent strain carrying an antibiotic resistance marker, which implies that this gene does not play a significant role in systemic *Salmonella* infection of the mouse.

Table 4. Virulence of *S. typhimurium* strains in mice.

Strain	Genotype	Mouse survival after inoculation ^a with bacterial strain	Mouse survival after inoculation ^a with mutant + complementing plasmid	Competitive index <i>in vivo</i>
NCTC120 23	wild-type	0/5	n.d.	0.98 ^b
MvP101	$\Delta sseD::aphT$	5/5	n.d.	>0.01
MvP102	$\Delta sseEsscB::aphT$	4/4	n.d.	0.79
MvP103	$sseC::aphT$	5/5	0/5	>0.01 (oral) >0.01 (i.p.)

^a Mice were inoculated intraperitoneally with 1×10^4 cells of each strain

^b Result of competition between wild-type strain NCTC12023 and a virulent mTn5 mutant identified in the STM screen.

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Example 5: Vaccination with the $sseC::aphT$, and $\Delta sseD::aphT$ mutant *S. typhimurium* strains MvP103 and MvP101

Strains carrying non-polar mutations as live vaccine carriers

To confirm the suitability of the MvP101 and MvP103 mutants as live vaccine carriers their level of attenuation was evaluated by determining the LD₅₀ after oral inoculation in mice. Groups of 10 mice were fed with serial dilutions of either MvP101, MvP103 or the wild-type parental strain NCTC12023 and dead animals were recorded within a period of 10

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days postinfection. The obtained results demonstrated that both mutants are highly attenuated when given orally to BALB/c mice (LD_{50} above 10^9) when compared with the parental strain ($LD_{50} = 6.9 \times 10^5$ CFU).

After intraperitoneal inoculation the LD_{50} of *S. typhimurium* NCTC12023 wild-type in BALB/c is 6 bacteria, and the LD_{50} of MvP103 in BALB/c is 2.77×10^6 after intraperitoneal inoculation. The mutation can be complemented by *psseC*, but no LD_{50} determination for the complemented mutant strain was performed. LD_{50} of MvP101 in BALB/c is 3.54×10^6 after intraperitoneal inoculation. A partial complementation by plasmid p5-K1 was possible. An intraperitoneal LD_{50} for MvP101 [p5-K1] of 8.45×10^2 was determined. (Description of p5-K1: a 3.2kb PstI fragment of p5-2 containing *sseC'sseDsseEsscBsseF'* was subcloned in low copy number cloning vector pWSK29).

Determination of the LD_{50}

Doses ranging from 10^5 to 10^9 CFU of either *S. typhimurium* NCTC12023 (wild-type) or the mutants MvP103 and MvP101 were orally inoculated into groups of 10 mice and survival was recorded over 10 days.

LD_{50} of *S. typhimurium* wild-type and mutant strains MvP101 and MvP103 after intraperitoneal infection was determined by inoculation of doses ranging from 10^1 to 10^7 CFU into groups of 5 female BALB/c mice of 6-8 weeks of age. Survival was recorded over a period of three weeks. The LD_{50} dose of the challenge strains was calculated by the method of Reed and Muench (Reed and Muench, 1938).

Immunization protocols

For vaccination, bacteria were grown overnight until they reach medium log phase. Then, they were harvested by centrifugation (3,000 x g) and resuspended in 5% sodium bicarbonate. Mice were immunized four times at 15 day intervals by gently feeding them with the bacterial suspension (10⁹ CFU/mouse) in a volume of approximately 30 µl. Control mice were vaccinated with the carrier, lacking plasmid.

Cytotoxicity assay

Spleen cells were obtained from mice 14 days after the last immunization and 2x10⁶ effector cells were restimulated *in vitro* for 5 days in complete medium supplemented with 20 U/ml of rIL-2 and 20 µM of the βGP1 peptide (β-gal p876-884, TPHPARIGL), which encompasses the immunodominant H-2L^d-restricted β-gal epitope. After restimulation, the assay was performed using the [³H]-thymidine incorporation method. In brief, 2x10⁶ of P815 cells per ml were labelled with [³H]-thymidine for 4 h in either complete medium or complete medium supplemented with 20 µM of βGP1 peptide and used as target cells. Following washing, 2x10⁵ labelled targets were incubated with serial dilutions of effector cells in 200 µl of complete medium for 4 h at 37°C. Cells were harvested and specific lysis was determined as follows: [(retained c.p.m. in the absence of effectors) - (experimentally retained c.p.m. in the presence of effectors) / retained c.p.m. in the absence of effectors] x 100.

Example 6: Evaluation of the induced immune response

Induction of mucosal immune responses after oral vaccination

To achieve protection against mucosal pathogens using live *Salmonella* carriers, elicitation of an efficient mucosal response is highly desirable.

Therefore, the presence of β -gal-specific antibodies in intestinal washes from mice immunized with either MvP101, MvP103 or SL7207 carrying pAH97 was investigated 52 days after immunization. As shown in Fig. 5., immunization with all three carriers stimulate the production of significant amounts of β -gal-specific IgA and, to a lesser extent, favor the transudation of antigen-specific IgG in the intestinal lumen. No statistically significant differences were observed among the mucosal responses to the different recombinant clones.

Cellular immune responses triggered after oral immunization with sseC and sseD mutants expressing β -gal

To evaluate the efficacy of the antigen-specific T cell responses generated in immunized mice, spleen cells were enriched in CD4+ T cells and restimulated *in vitro* during four days with β -gal. As shown in Fig. 6, although antigen-specific CD4+ -enriched spleen cells were generated after vaccination with the three carriers, MvP103 and MvP101 were significantly more efficient than SL7207 ($P < 0.05$) at triggering specific cellular immune response. In contrast, cells isolated from mice immunized with the carrier alone failed to proliferate in the presence of β -gal.

To investigate the Th-type of immune response triggered by immunization, the content of IFN- γ , IL-2, IL-4, IL-5, IL-6 and IL-10 was measured in the supernatant fluids of restimulated cells. The results demonstrated that a predominant Th1 response pattern was induced in mice immunized with all the carriers. IFN- γ was the only cytokine with significantly increased levels in comparison to those observed in supernatants from spleen cells isolated from mice immunized with plasmidless carriers (Fig. 7). Interestingly, in agreement with the IgG isotype patterns, the levels of IFN- γ detected in

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supernatants from cells of mice immunized with MvP103 [pAH97] were significantly higher ($P < 0.05$) than those from animals receiving either MvP101 [pAH97] or SL7207 [pAH97] (Fig. 7).

- 5 Antigen-specific antibody responses generated in mice orally immunized with the attenuated *S. typhimurium* vaccine carriers expressing the model antigen β -gal

Groups of mice were immunized with the recombinant strains MvP101 [pAH97] and MvP103 [pAH97]. To estimate the efficacy of the prototypes another group was vaccinated with the well-established carrier strain SL7207 [pAH97]. The abilities of the different carriers to induce a systemic humoral response was determined by measuring the titer of β -gal-specific antibodies in the serum of vaccinated mice. As shown in Fig. 8, significant
10 titers of β -gal-specific IgG and IgM antibodies were detected at day 30 in all vaccinated animals. In contrast to the IgM titers which reach a plateau at day 30, the titers of IgG steadily increased until day 52 from immunization when the experiment was concluded. Although all tested
15 carriers exhibit an excellent performance, the MvP103 mutant was the most efficient at inducing anti- β -gal IgG antibodies ($P < 0.05$). No significant levels of β -gal-specific IgA were detected in mice immunized with any of the three recombinant clones (data not shown).
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To determine the subclass distribution of the anti- β -gal IgG, serum samples
25 were analyzed for specific levels of IgG1, IgG2a, IgG2b and IgG3. The results shown in Fig. 9 demonstrate that the main β -gal-specific IgG isotype present in sera of all immunized mice was IgG2, suggesting of a predominant Th1 response. Interestingly, a lower concentration of IgG1 ($P < 0.05$) was observed in mice immunized with MvP103 than in those

receiving MvP101 and SL7202, indicating a similar response pattern in animals immunized with the last two carriers.

5 *Sample collection*

Serum samples were collected at different time points and monitored for the presence of β -gal-specific antibodies. At day 52 after immunization, intestinal lavages were obtained by flushing the small intestine with 2 ml of
10 PBS supplemented with 50 mM EDTA, 0.1 % bovine serum albumin and 0.1 mg/ml of soybean trypsin inhibitor (Sigma). Then, the lavages were centrifuged (10 min at 600 x g) to remove debris, supernatants were removed and supplemented with phenylmethylsulfonyl fluoride (10 mM) and NaN_3 , and stored at -20°C .

15

Antibody assays

Antibody titres were determined by an enzyme-linked immunosorbent assay
20 (ELISA). Briefly, 96 well Nunc-Immuno MaxiSorpTM assay plates (Nunc, Roskilde, Denmark) were coated with 50 μl /well β -gal (5 $\mu\text{g}/\text{ml}$) in coating buffer (0.1 M Na_2HPO_4 , pH 9.0). After overnight incubation at 4°C , plates were blocked with 10% FCS in PBS for 1 h at 37°C . Serial two-fold dilutions of serum in FCS-PBS were added (100 μl /well) and plates were
25 incubated for 2 h at 37°C . After four washes with PBS-0.05% Tween 20, secondary antibodies were added: biotinylated γ -chain specific goat anti-mouse IgG, μ -chain specific goat anti-mouse IgM, α -chain specific goat anti-mouse IgA antibodies (Sigma, St. Louis, MO) or, to determine IgG subclass, biotin-conjugated rat anti-mouse IgG1, IgG2a, IgG2b and IgG3 (Pharmingen)
30 and plates were further incubated for 2 h at 37°C . After four washes, 100

5 μ l of peroxidase-conjugated streptavidin (Pharmingen, St. Diego, CA) were added to each well and plates were incubated at room temperature for 1 h. After four washes, reactions were developed using ABTS [2,2'-azino-bis-(3-ethybenzthiazoline-6-sulfonic acid)] in 0.1 M citrate-phosphate buffer (pH 4.35) containing 0.01% H₂O₂. Endpoint titers were expressed as the reciprocal log₂ of the last dilution which gave an optical density at 405 nm 0.1 unit above the values of the negative controls after a 30 min incubation.

10 To determine the concentration of total Ig present in the intestinal lavages, serial dilutions of the corresponding samples were incubated in microtiter plates that had been coated with goat anti-mouse IgG, IgM and IgA as capture antibodies (100 μ g/well, Sigma) and serial dilutions of purified mouse IgG, IgM and IgA (Sigma) were used to generate standard curves.
15 Detection of antigen-specific Ig was performed as described above.

Induction of antigen-specific CTL responses in mice orally immunized with the carrier strains expressing β -gal

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The elicitation of MHC class I restricted responses are particularly important for protection against many intracellular pathogens and tumors. It has been shown that antigen-specific CD8 + CTL can be generated both *in vitro* and *in vivo* after immunization with recombinant *Salmonella* spp. expressing heterologous antigens. Therefore, we considered it important to determine
25 whether the tested carriers were also able to trigger a β -gal-specific CTL response. Spleen cells were collected from mice vaccinated with either MvP101 [pAH97], MvP103 [pAH97] or SL7207 [pAH97] at day 52 from immunization and restimulated *in vitro* with β GP1-pulsed syngenic spleen
30 cells for 5 days. As shown in Fig. 10, the spleen cells from mice immunized

with either of the three constructs induced significant lysis of β GP1-loaded target cells compared with unloaded controls. The more efficient responses were observed using the carrier strain MvP103. The lysis was mediated by CD8 + T cells since the cytotoxic activity was completely abrogated when
5 CD8 + T effector cells were depleted (data not shown).

Cytokine determination

10 Culture supernatants were collected from proliferating cells on days 2 and 4, and stored at -70°C. The determination of IL-2, IL-4, IL-5, IL-6, IL-10 and IFN- γ was performed by specific ELISA. In brief, 96-well microtiter plates were coated overnight at 4°C with purified rat anti-mouse IL-2 mAb (clone JESG-1A12), anti-IL-4 mAb (clone 11B11), anti-IL-5 mAb (clone
15 TRFK5), anti-IL-6 mAb (clone MP5-20F3), anti-IL-10 mAb (clone JES5-2A5), and anti-IFN- γ mAb (clone R4-6A2) (Pharmingen). After three washes, plates were blocked and two-fold dilutions of supernatant fluids were added. A standard curve was generated for each cytokine using recombinant murine IL-2 (rIL-2), rIL-4, rIL-5, rIL-6, rIFN- γ , and rIL-10
20 (Pharmingen). Plates were further incubated at 4°C overnight. After washing, 100 μ l/well of biotinylated rat anti-mouse IL-2 (clone JES6-5H4), IL-4 (clone BVD6-24G2), IL-5 (clone TRFK4), IL-6 (clone MP5-32C11), IL-10 (clone SXC-1) and INF- γ (clone XMG1.2) monoclonal antibodies were added and incubated for 45 min at RT. After six washes, streptavidin-peroxidase
25 conjugated was added and incubated for 30 min at RT. Finally, the plates were developed using ABTS.

30 *Depletion of CD8 + spleen cells.*

The CD8+ cell subset was depleted using MiniMACS Magnetic Ly-2 Microbeads according to the manufacturer's instructions (Miltenyi Biotec). Depleted cell preparations contained 1 % CD8+ cells.

5

FACScan analysis

Approximately 5×10^5 cells were incubated in staining buffer (PBS supplemented with 2% FCS and 0.1% sodium azide) with the desired
10 antibody or combination of antibodies for 30 min at 4°C. After washes, cells were analysed on a FACScan (Becton Dickinson). The monoclonal antibodies used were FITC-conjugated anti-CD4 and anti-CD8 (clones H129.19 and 53-6.7; Pharmingen).

15

Example 7: Cell proliferation

Cell proliferation assay

20 Spleen cell suspensions were enriched for CD4+ T cells using MiniMACS Magnetic Ly-2 and indirect goat-anti-mouse-IgG Microbeads according to the instructions of the manufacturer (Miltenyi Biotec GmbH, Germany). Cell preparations contained > 65% of CD4+ cells. Cells were adjusted to 2×10^5 cells/ml in complete medium supplemented with 20 U/ml of mouse
25 rIL-2 (Pharmingen), seeded at 100 μ l/well in a flat-bottomed 96-well microtiter plate (Nunc, Roskilde, Denmark) and incubated for four days in the presence of different concentrations of soluble β -gal. During the final 18 hours of culture 1 μ Ci of [3 H]-thymidine (Amersham International, Amersham, U.K.) was added per well. The cells were harvested on paper filters using a cell
30 harvester and the [3 H]-thymidine incorporated into the DNA of proliferating cells was determined in a β -scintillation counter.

Example 8: Characterization of *ssr* genes and construction and characterization of the *ssr* mutant *S. typhimurium* strains MvP284 , MvP320 and MvP333

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Homology of the two component regulator genes ssrA and ssrB of SPI2 with other bacterial proteins

The SPI2 gene *ssrA* encodes a protein similar to sensor components of bacterial two component regulatory systems as has been described before (Ochman *et al.*, 1996). For consistency with the nomenclature of SPI2 virulence genes (Hensel *et al.*, 1997b; Valdivia and Falkow, 1997), this gene is designated *ssrA*. Downstream of *ssrA*, an ORF with coding capacity for a 24.3 kDa protein was identified. This gene shares significant similarity with a family of genes encoding transcriptional activators like DegU of *Bacillus subtilis*, UvrY of *E. coli* and BvgA of *Bordetella pertussis*. Therefore, it is likely that the protein acts as the regulatory component of the *ssr* system and the gene was designated *ssrB*.

20

Inverse regulation of SPI1 and SPI2

The expression of the type III secretions systems of SPI1 and SPI2 is tightly regulated by environmental conditions. While SPI1 is induced during late log/early stationary phase after growth in rich media of high osmolarity and limiting O₂ (oxygen) concentration, no induction of SPI2 gene expression was observed. In contrast, after growth in minimal medium with limiting amounts of Mg²⁺ (8 μM) the *ssaB::luc* fusion was highly expressed while the *sipC::lacZ* fusion was not expressed. The expression of the *ssaB::luc* fusion is dependent on the function of SsrA/B, since there is no expression in the *ssrB*-negative background strain P8G12 (Hensel *et al.*, 1998). The expression of the *sipC::lacZ* fusion is dependent on HilA, the transcriptional

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regulator of SPI1. We also observed that a mutation in *ssrB* affects expression of the *sipC::lacZ* fusion. This indicates that SPI2 has a regulatory effect on the expression of SPI1 genes.

5 Bacterial strains harbouring a *luc* fusion to *ssaB* in SPI2 (strain MvP131) and a *lacZ* fusion to *sipC* in SPI1 (strain MvP239) were grown under conditions previously shown to induce SPI gene expression. Bacteria were grown over night in minimal medium containing 8 μ M Mg^{2+} or over night in LB broth containing 1 % NaCl (LB 1%NaCl). The *Luc* activity of strain MvP131 and
10 β -galactosidase activity of strain MvP239 were determined. As a control, both reporter fusions were assayed in the *ssrB* negative strain background of P8G12.

Expression levels of *lacZ* reporter-gene fusions to SPI genes were assayed
15 as described by Miller, 1992.

Construction and analysis of *sseA* reporter gene fusion

20 A 1.1kb *SmaI/HincII* fragment of p5-4 was subcloned into pGPL01, a suicide vector for the generation of *luc* fusions (Gunn and Miller, 1996). The resulting construct, in which 1.0kb upstream and 112 bp of *sseA* is transcriptionally fused to *luc* was used to transform *E. coli* S17-1 Δ *pir*, and conjugational transfer to *S. typhimurium* performed as described previously
25 (Gunn and Miller, 1996). Strains that had integrated the reporter gene fusion into the chromosome by homologous recombination were confirmed by PCR and Southern hybridization analysis. Subsequently, the fusion was moved by P22 transduction into the wild-type and various mutant strain backgrounds with mTn5 insertions in SPI1 or SPI2 genes (Maloy *et al.*,
30 1996). As a control, a strain was constructed harbouring a chromosomal integration of pLB02, a suicide plasmid without a promoter fusion to the *luc* gene (Gunn and Miller, 1996). For the analysis of gene expression, strains

were grown for 16 h in minimal medium with aeration. Aliquots of the bacterial cultures were lysed and luciferase activity was determined using a luciferase assay kit according to the manufacturer's protocol (Boehringer Mannheim). Photon detection was performed on a Microplate scintillation/luminescence counter (Wallac, Turku). All assay were done in triplicate, and replicated on independent occasions.

Expression of *sseA* is dependent on SsrAB

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To establish if the *sse* genes are part of the SPI2 secretion system, the expression of an *sseA::luc* reporter gene fusion, integrated by homologous recombination into the chromosome of different SPI2 mutant strains, has been investigated (Fig. 11). Transcriptional activity of *sseA* in a wild-type background during growth in minimal medium was dramatically reduced by inactivation of the SPI2 two-component system. Transposon insertions in *ssrA* (mutant strain P3F4) and *ssrB* (mutant strain P8G12), encoding the sensor component and the transcriptional activator, respectively, resulted in 250 to 300-fold reduced expression of *sseA*. Inactivation of *hilA*, the transcriptional activator of SPI1 (Bajaj *et al.*, 1996), had no effect on *sseA* gene expression. Transposon insertions in two genes encoding components of the SPI2 type III secretion apparatus (*ssaJ::mTn5* and *ssaT::mTn5*; mutant strains P11D10 and P9B7; Shea *et al.*, 1996) also had no significant effect on the expression of *sseA*. These data show that SsrA/B is required for the expression of *sseA*, but that *hilA* is not.

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Expression of SPI2 genes within macrophages is dependent on SsrA/B

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The presence of *S. typhimurium* within eukaryotic cells (macrophages) induces the expression of SPI2 genes as indicated by analysis of fusions to

ssaB and *ssaH*. This expression is dependent on the two component regulatory system SsrA/B encoded by SPI2.

The murine macrophage-line cell line J744 was used for this experiment. Macrophages were infected at a multiplicity of infection of 10 bacteria per macrophage with MvP131 (*luc* fusion to *ssaB*), MvP266 (*luc* fusion of *ssaH*) and MvP244 (*luc* fusion to *ssaB* in a *ssrB* negative background). Extracellular bacteria were killed by the addition of gentamicin (20 µg/ml). At various time points, macrophages were lysed by the addition of 0.1% Triton X-100, and intracellular bacteria were enumerated by plating serial dilutions onto LB agar plates. A further aliquot of the bacteria was recovered and the luciferase activity was determined. Luciferase activities were expressed as a relative light emission per bacteria.

Effects of a mutation in *ssrB* on the secreted effector protein of SPI1 SipC

Analysis of proteins secreted into the growth medium by the *S. typhimurium* SPI2 mutant strain MvP320 (non-polar mutation in *a*, Fig. 12) revealed the absence or strong reduction in the amounts of the secreted SPI1 effector protein (Hensel *et al.*, 1997b). These SPI2 mutants are also reduced in their ability to invade cultured epithelial cells or cultured macrophages (Hensel *et al.*, 1997b). To examine this phenomenon in greater detail, we expressed recombinant SipC (rSipC) and raised antibodies against rSipC in rabbits. In Western blots, antiserum against rSipC reacted with a 42 kDa protein from precipitates of culture supernatants of *S. typhimurium* wild-type strain NCTC12023. No reaction was observed with supernatants from cultures of EE638, a strain deficient in SipC (Hueck *et al.*, 1995). Furthermore, in Western blots SipC could not be detected in culture supernatants of the SPI2 mutants MvP320. However, SipC was detected in culture supernatants of other SPI2 mutants like P2D6 (*ssaV::mTn5*), P9B6 (*ssaV::mTn5*) and NPssaV (*ssaV::aphT*) (Deiwick *et al.*,

1998). The detection by antiserum of SipC in culture supernatants of various strains was in accord with the presence or absence of SipC as detected by SDS-PAGE. Further it was analyzed whether the absence of SipC in culture supernatants of SPI2 mutant strains was due to defective secretion of SipC via the type III secretion system or reduced synthesis of SipC in these strains. Antiserum against rSipC was used to detect SipC in pellets of cultures grown under inducing conditions for the expression of SPI1 genes (i.e. stationary phase, high osmolarity, low oxygen) (Bajaj *et al.*, 1996). Analysis of wild-type and strains carrying various mutations in SPI1 and SPI2 genes indicated highly reduced amounts of SipC in the mutants with a non-polar mutation in *ssrB*. However, SipC was detected at levels comparable to those observed in pellets of wild-type cultures and SPI2 mutant strains P2D6, P9B6 and NPss α V. The effect on SipC synthesis is not due to reduced growth rates or reduced protein levels in SPI2 mutants, since both parameters were comparable for the wild-type and SPI2 mutants.

Effects of a mutation in the SPI2 gene *ssrB* on the expression of SPI1 genes

In order to assay the effect of SPI2 mutations on the expression of SPI1 genes, previously characterized fusions of *lacZ* to various SPI1 genes (Bajaj *et al.*, 1995; Bajaj *et al.*, 1996) were transduced into the SPI2 mutant MvP320 and various SPI1 mutants to generate a set of reporter fusion strains. The expression of the reporter β -galactosidase in cultures grown under conditions inducing for SPI1 expression (see above) was assayed. A Tn insertion in *hilA* (P4H2) reduced the expression of *prgK* as well as *sipC*, while an insertion in *spaRS* (P6E11) only affected the expression of *sipC*. Some mutant strains with a mutation in the SPI2 gene *ssrB* encoding a components of the two component regulatory system showed reduced expression of reporter fusions to *prgK* and *sipC* (Fig. 11). The effects on the expression of both genes was similar. Other mutant strains with Tn

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insertions in *ssaV* (P2D6, P9B6), as well as mutant NP*ssaV* harbouring a non-polar insertions in *ssaV*, had levels of expression of *prgK* and *sipC* comparable to that of corresponding reporter fusions in a wild-type genetic background. Analysis of *lacZ* fusions to *prgH* and *invF* revealed a similar effect on expression as shown for *prgK* and *sipC*.

A mutation in the SPI2 gene *ssrB* affects expression of the SPI1 regulator *hilA*

Analysis of reporter fusions to *sipC* and *prgK* indicated that expression of genes in two different operons of SPI1 can be affected by SPI2 mutations, suggesting that these mutations affect other SPI1 genes involved in regulation of *sipC* and *prgK*. It has been demonstrated previously that the expression of SPI1 genes is under the control of the transcriptional activator HilA (Bajaj *et al.*, 1995; Bajaj *et al.*, 1996). The expression of *hilA* was therefore analyzed in the presence of a SPI2 mutation in *ssrB*. The SPI2 mutant strain MvP320 had largely diminished levels of *hilA* expression. Again, very low levels of *hilA* expression were observed in mutants that had reduced levels of *prgK* and *sipC* expression. To analyze whether the effect of the SPI2 mutation on *sipC* expression resulted from the reduced expression of *hilA*, we next performed complementation experiments in various mutant strains harbouring pVV135 (constitutive expression of *hilA*) (Bajaj *et al.*, 1996) or pVV214 (expression of *hilA* from the native promoter) (Bajaj *et al.*, 1995). In accordance with a previous study (Bajaj *et al.*, 1995), the *hilA* mutation of strain P4H2 was complemented by pVV214. However, the *sipC* expression was not restored in the mutant strain MvP320 harbouring either pVV135 or pVV214.

Construction of the *ssrA* and *ssrB* mutant *S. typhimurium* strains MvP284 and MvP320

- Mutant MvP284, *ssrA*. The *ssrA* gene (Fig. 12) was subcloned from the phage clone λ 2 derived plasmid p2-2 on a 5.7kb *Bam*HI fragment in pUC18 as indicated in Table 1. A 1.6kb fragment was recovered after *Hind*III and *Eco*RV digestion of p2-2 and subcloned in *Hind*III/*Hinc*II-digested pBluescript II KS+. The resulting construct termed p2-20 was digested with *Hinc*II and dephosphorylated with alkaline phosphatase. The *aphT* cassette was isolated as described above and ligated to the linearized plasmid p2-20 in the same orientation into the unique *Hinc*II site. After transformation of *E. coli* XL-1 Blue and selection against kanamycin and carbenicillin (50 μ g/ml each) one clone has been chosen and the harbouring plasmid isolated. This plasmid was termed p2-21 and its identity proved via restriction analysis. p2-21 was further digested with *Kpn*I and *Xba*I, a 2.5kb fragment isolated and ligated to *Kpn*I/*Xba*I-digested pKAS32. This plasmid was electroporated into *E. coli* CC118 λ pir and transformants selected to kanamycin and carbenicillin (50 μ g/ml each). As done before, one clone was chosen, its plasmid with the according DNA fragment in pKAS32, termed p2-22, isolated and confirmed by restriction analysis. Plasmid p2-22 was electroporated into *E. coli* S17-1 λ pir and transferred into *S. typhimurium* NCTC12023 (streptomycin resistant) by conjugation as has been described previously (de Lorenzo and Timmis, 1994). Exconjugants in which the *ssrA* gene had been replaced by the cloned gene disrupted by insertion of the *aphT* cassette were selected by its growth on M9 + glucose minimal medium agar plates (Maloy *et al.*, 1996) and its resistance to kanamycin and carbenicillin (100 μ g/ml). The resulting exconjugants were finally shown to have a lactose negative phenotype and to be sensitive to kanamycin and streptomycin. Selected clones were further examined by Southernblot

analysis. In order to exclude possible mutations which might have been developed during the cloning procedure the mutated *ssrA* allele was transferred into a fresh *Salmonella* background by P22 transduction (described by Maloy *et al.*, 1996). The resulting *Salmonella* strain MvP284 was examined for the presence of the resistance cassette within the *ssrA* gene by the use of primers *ssrA*-For (5'- AAG GAA TTC AAC AGG CAA CTG GAG G-3') and *ssrA*-Rev (5'- CTG CCC TCG CGA AAA TTA AGA TAA TA -3'). Amplification of DNA from clones containing the wild-type *ssrA* allele resulted in a PCR product of 2800 bp, use of DNA from clones harbouring a *ssrA* allele disrupted by the *aphT* cassette resulted in a PCR product of 3750bp. The resulting *Salmonella* strain MvP320 was examined for the presence of the resistance cassette within the *ssrB* gene by the use of Southern hybridization analysis of total DNA of exconjugants.

Mutant MvP320, *ssrB*. The *ssrB* gene (Fig. 12) was subcloned from the phage clone λ 1 derived plasmid p1-6 on a 4.8kb *Pst*I/*Bam*HI-fragment in pT7-Blue as indicated in Table 1. A 1.7kb fragment was recovered after *Bam*HI and *Hinc*II digestion of p1-6 and subcloned in *Bam*HI/*Hinc*II-digested pBluescript II KS+. The resulting construct termed p1-20 was digested with *Eco*RV and dephosphorylated with alkaline phosphatase. The *aphT* cassette was isolated as described above and ligated to the linearized plasmid p1-20 in the same orientation into the unique *Eco*RV site. After transformation of *E. coli* XL-1 Blue and selection against kanamycin and carbenicillin (50 μ g/ml each) one clone has been chosen and the harbouring plasmid isolated. This plasmid was termed p1-21 and its identity confirmed by restriction analysis. p1-21 was further digested with *Kpn*I and *Xba*I, a 2.5kb fragment isolated and ligated to *Kpn*I/*Xba*I-digested pKAS32. This plasmid was electroporated into *E. coli* CC118 λ pir and transformed bacteria selected to kanamycin and carbenicillin (50

$\mu\text{g/ml}$ each) was performed. As done before, one clone was chosen, its plasmid with the according DNA fragment in pKAS32, termed p1-22, isolated and confirmed by restriction analysis. Plasmid p1-22 was electroporated into *E. coli* S17-1 *Ap^r* and transferred into *S. typhimurium* NCTC12023 (streptomycin resistant) by conjugation as has been described previously (de Lorenzo and Timmis, 1994). Exconjugants in which the *ssrB* gene had been replaced by the cloned gene disrupted by insertion of the *aphT* cassette were selected by its growth on M9 + glucose minimal medium agar plates (Maloy *et al.*, 1996) and its resistance to kanamycin and carbenicillin (100 $\mu\text{g/ml}$). The resulting exconjugants were finally shown to have a lactose negative phenotype and to be sensitive to kanamycin and streptomycin. Selected clones were further examined by Southernblot analysis. In order to exclude possible mutations which might have been acquired during the cloning procedure the mutated *ssrB* allele has been transferred into a fresh *Salmonella* background by P22 transduction (described by Maloy *et al.*, 1996). Screening of mutants with a insertion of the *aphT* cassette within the *ssrB* locus was performed by PCR using primers *ssrB*-For (5'- CTT AAT TTT CGC GAG GG -3') and *ssrB*-Rev (5'- GGA CGC CCC TGG TTA ATA -3'). Amplification of DNA from clones containing the wild-type *ssrB* allele resulted in a PCR product of 660 bp, use of DNA from clones harbouring a *ssrB* allele disrupted by insertion of the *aphT* cassette resulted in a PCR product of 1600 bp. The resulting *Salmonella* strain MvP320 was examined for the presence of the resistance cassette within the *ssrB* gene by the use of Southern hybridization analysis of total DNA of exconjugants.

Construction of the mutant strain MvP340 carrying an in-frame deletion in *ssrA*

A deletion of 407 codons between codon 44 and 451 of *ssrB* was generated. Plasmid p2-2 was digested by *Bam*HI and *Kpn*I, a fragment of 3.7kb was recovered and subcloned in pBluescript KS+ to generate p2-50. Plasmid p2-50 was linearized by digestion with *Pst*I, which cuts once within the subcloned fragment of the *ssrA* gene. Primers *ssrA*-del-1 (5'- GGT CTG CAG GAT TTT TCA CGC ATC GCG TC -3') and *ssrB*-del-2 (5'- GGT CTG CAG AAC CAT TGA TAT ATA AGC TGC -3') were designed to introduce *Pst*I sites. PCR was performed using linearized p2-50 as template DNA. The TaqPlus polymerase (Stratagene) was used according to the instructions of the manufacturer. Reactions of 100 μ l volume were set up using 10 μ l of 10 x TaqPlus Precision buffer containing magnesium chloride, 0.8 μ l of 100 mM dNTPs, 250 ng DNA template (linearized p2-50), 250 ng of each primer and 5 U of TaqPlus DNA polymerase. PCR was carried out for 35 cycles of: 95°C for 1 minute, 60°C for 1 minute, 72°C for 6 minutes. Then a final step of 72°C for 10 minutes was added. 10 μ l of the PCR reaction were analyzed. A product of the expected size was recovered, digested by *Pst*I, self-ligated, and the ligation mixture was used to transform *E. coli* DH5 α to resistance to carbenicillin. Plasmids were isolated from transformants and the integrity of the insert and the deletion was analyzed by restriction analysis and DNA sequencing. The insert of a confirmed construct was isolated after digestion with *Xba*I and *Kpn*I and ligated to *Xba*I/*Kpn*I-digested vector pKAS32. The resulting construct was used to transform *E. coli* S17-1 λ pir to resistance to carbenicillin, and conjugational transfer of the plasmid to *S. typhimurium* (Nal^R, Strep^R) was performed according to standard procedures (de Lorenzo and Timmis, 1994). Exconjugants that had integrated the suicide plasmid by homologous recombination were selected by resistance to nalidixic acid and carbenicillin, and screened for sensitivity to streptomycin. Such clones were grown in LB to OD600 of about 0.5 and aliquots were plated on LB containing 250 μ g/ml streptomycin to select for

colonies which had lost the integrated plasmid and undergone allelic exchange. Clones resistant to streptomycin but sensitive to carbenicillin were used for further analysis. Screening of mutants with a deletion within the *ssrA* locus was performed by PCR using primers *ssrA*-For (5'- AAG GAA
5 TTC AAC AGG CAA CTG GAG G-3') and *ssrA*-Rev (5- CTG CCC TCG CGA
AAA TTA AGA TAA TA -3'). Amplification of DNA from clones containing the wild-type *ssrA* allele resulted in a PCR product of 2800 bp, use of DNA from clones harbouring a *ssrA* allele with an internal deletion resulted in a PCR product of 1580 bp. The integrity of clones harbouring the *ssrA*
10 deletion was further confirmed by Southernanalysis of the *ssrA* locus. Finally, the *ssrA* locus containing the internal in-frame deletion was moved into a fresh strain background of *S. typhimurium* by P22 transduction (Maloy *et al.*, 1996) and the resulting strain was designated MvP340.

15 Southern hybridization

Genomic DNA of *Salmonella* was prepared as previously described (Hensel *et al.*, 1997). For Southern hybridization analysis, genomic DNA was digested with *EcoRI* or *EcoRV*, fractionated on 0.6 % agarose gels and
20 transferred to Hybond N⁺ membranes (Amersham, Braunschweig). Various probes corresponding to the *ssrA* and *ssrB* region were obtained as restriction fragments of the subcloned insert of λ 1 and λ 2.

25 Example 9: Evaluation of safety of *S. typhimurium* strain MvP320

For competition assays between *S. typhimurium* wild-type and the mutant strain MvP320, bacteria were grown in LB to an optical density at 600 nm of 0.4 – 0.6. Cultures were diluted and aliquots of the two cultures were
30 mixed to form an inoculum containing equal amounts of both strains. The ratio of both strains was determined by plating dilutions on LB plates containing antibiotics selective for individual strains. An inoculum of about

10⁴ colony forming units (cfu) was used to infect 6 to 8 weeks old female BALB/c mice (Charles River Breeders, Wiga) by injection into the peritoneal cavity. At several time points after infection mice were sacrificed by cervical dislocation and the bacterial load of liver and spleen was
5 determined by plating tissue homogenates using the 'WASP' (Meintrup, Lähden) spiral plating device. Plating was performed using LB plates containing 50 µg/ml kanamycin or 100 µg/ml nalidixic acid to select for the mutant strains or the wild-type, respectively.

10 Strain MvP320 harbouring the *aphT* gene cassette in *ssrB* was recovered in at least 1000-fold lower numbers than the *S. typhimurium* wild-type strain. These data indicate that *ssrB* contributes significantly to systemic infections of *S. typhimurium* in the mouse model of salmonellosis.

15

Statistical analysis of all experiments.

Statistical significance between paired samples was determined by Student's *t* test. The significance of the obtained results was determined
20 using the statgraphic plus for windows 2.0 software (Statistical Graphic Corp.).

Example 10: Characterization of the in vivo inducible P_{ssaE} Promoter (Promoter B, Fig.24B)

25

The promoter which is located upstream of *ssaE* (P_{ssaE}, formerly called Promoter B) was shown to be regulated by the *ssrAB* locus. A DNA fragment comprising nucleotide 800 to 120 (800-1205) in the included sequence (Fig.21A) was shown to confer *ssrB*-dependent regulation upon
30 the expression of a reporter gene (gfp) fused to the promoter. The DNA fragment was cloned on a low-copy plasmid in front of the gfp gene. As has been shown previously for other reporter gene constructs, induction of

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expression from P_{ssaE} (800-1205) was observed in magnesium minimal medium (Deiwick et al., 1999) and was dependent on the presence of a chromosomal wild type allele of *ssrB*. A shorter DNA fragment, comprising nucleotide 923 to 1205 (923-1205) in the included sequence, did not
5 confer regulation upon expression of gfp. However, expression was reduced compared to the P_{ssaE} (800-1205) fragment and was not induced in magnesium minimal medium nor was it dependent on *ssrB*. Thus, the P_{ssaE} (800-1205) fragment comprises promoter active and regulatory sequences, probably including an SsrB-binding site.

Description of the drawings

Fig. 1. Map of *Salmonella* Pathogenicity Island 2 (A) indicating the positions of the mutations in strains MvP101, MvP102, and MvP103 (B). A partial restriction map of the genomic region is shown, and the positions of plasmid inserts relevant for this work are indicated (C). B, *Bam*HI; C, *Cl*al; E, *Eco*RI; P, *Pst*I; V, *Eco*RV; S, *Sma*I; EMBL database accession numbers are indicated for the sequences in (A).

Fig. 2a. Alignment of the deduced SseB amino acid sequence to EspA of EPEC (Elliot *et al.*, 1998). The ClustalW algorithm of the MacVector 6.0 program was used to construct the alignments. Similar amino acid residues are boxed, identical residues are boxed and shaded.

Fig. 2b. Alignment of the deduced SseC amino acid sequence to EspD of EPEC (Elliot *et al.*, 1998), YopB of *Yersinia enterocolitica* (Hakansson *et al.*, 1993), and PepB of *Pseudomonas aeruginosa* (Hauser *et al.*, 1998). The ClustalW algorithm of the MacVector 6.0 program was used to construct the alignments. Positions where at least three amino acid residues are similar are boxed, where at least three residues are identical are boxed and shaded.

Fig. 3. Intracellular accumulation of *S. typhimurium* SPI2 mutants in RAW 264.7 macrophages. Following opsonization and infection, macrophages were lysed and cultured for enumeration of intracellular bacteria (gentamicin protected) at 2 h and 16 h post-infection. The values shown represent the fold increase calculated as a ratio of the intracellular bacteria between 2 h and 16 h post-infection. Infection was performed in triplicates for each strain and the standard error from the mean is shown.

Fig. 4. Intracellular survival and replication of SPI2 mutant *S. typhimurium* in (A) J774.1 cells and (B) periodate-elicited peritoneal macrophages from C3H/HeN mice. After opsonization and internalization, phagocytes were lysed and cultured for enumeration of viable intracellular bacteria at time 0 h. The values shown represent the proportion of this intracellular inoculum viable at 20 h \pm the standard error of the mean. Samples were processed in triplicate, and each experiment was performed at least twice.

Fig. 5. β -gal-specific antibodies in intestinal lavages of mice orally immunized with either MvP101[pAH97], MvP103 [pAH97], SL7207 [pAH97] or MvP101 at day 52 after immunization. Results are expressed as percentage of the corresponding total Ig subclass present in the intestinal lavage, the SEM is indicated by vertical lines. Significant levels of antigen-specific IgM could not be detected in any of the groups. The results obtained with MvP103 and SL7207 (not shown) were similar to those for MvP101.

Fig. 6. β -gal-specific proliferative response of CD4 + enriched spleen cells from mice orally immunized with either MvP101 [pAH97], MvP103 [pAH97], SL7207 [pAH97] or MvP101. Cells were restimulated *in vitro* during a 4 day incubation with different concentrations of soluble β -gal. The values are expressed as mean cpm of triplicates; the SEM was in all cases lower than 10%. Background values obtained from wells without the stimulating antigen were subtracted. Results obtained with MvP103 and SL7207 (not shown) were similar to those obtained with MvP101.

Fig. 7. IFN- γ present in supernatants from cultured CD4 + enriched spleen cells of mice orally immunized with either MvP101 [pAH97], MvP103 [pAH97], SL7207 [pAH97] or plasmidless MvP101 at day 2 and 4 of culture. Spleen cells were isolated from mice at day 52 after immunization, and CD4 + enriched populations were restimulated *in vitro* for four days in the presence of soluble β -gal (20 μ g/ml). IFN- γ production was determined

by ELISA, results represent the means of three determinations. The SEM is indicated by vertical lines, similar results were obtained using any of the plasmidless carriers (not shown). No significant differences with the control groups were observed when IL-2, IL-4, IL-5, IL-6 and IL-10 were tested (not shown).

Fig. 8. Kinetics of the β -gal-specific serum IgG (closed symbols) and IgM (open symbols) antibody responses in mice ($n = 5$) after oral immunization with either MvP101 [pAH97] (triangle), MvP103 [pAH97] (circle), SL7207 [pAH97] (square) or plasmidless MvP101 (diamond). Results are expressed as the reciprocal \log_2 of the geometric mean end point titer (GMT), the SEM was in all cases lower than 10%. Similar results were obtained using any of the plasmidless carriers (not shown), immunizations are indicated by arrows.

Fig. 9. Subclass profiles of the β -gal-specific IgG antibodies present in the serum of mice ($n = 5$) orally immunized with either MvP101 [pAH97], MvP103 [pAH97], SL7207 [pAH97] or plasmidless MvP101 at day 52 post-immunization. Results are expressed as ng/ml, the SEM is indicated by vertical lines. Similar results were obtained using any of the plasmidless carriers (not shown).

Fig. 10. Recognition of the MHC class I-restricted β GP1 epitope by lymphocytes primed *in vivo* in mice by oral vaccination with either MvP101 [pAH97], MvP103 [pAH97], SL7207 [pAH97] or plasmidless MvP101. Spleen cells from immunized mice were restimulated *in vitro* five days in the presence of 20 μ M β GP1. At the end of the culture, lymphocytes were tested in a [3 H]-thymidine-release assay using P815 (open symbols) and β GP1-loaded P815 (closed symbols) as targets. Results are mean values of triplicate wells (one out of three independent experiments is shown) and are expressed as: [(retained cpm in the absence of effectors) - (experimentally retained cpm in the presence of effectors) / retained cpm in the absence of

effectors] x 100; SEM were lower than 5% of the values. Similar results were obtained using any of the plasmidless carriers (not shown).

5 **Fig. 11.** Expression of an *sseA::luc* fusion in wild-type and mTn5 mutant strains of *S. typhimurium*.

10 **Fig. 12.** Map of *Salmonella* Pathogenicity Island 2 (A) indicating the positions of the mutations in strains MvP284 and MvP320 (B). A partial restriction map of the genomic region is shown, and the position of inserts of plasmids relevant for this work is indicated (C). B, *Bam*HI; C, *Cl*al; H, *Hind*III; P, *Pst*I; V; S, *Sma*I; *Eco*RV; II, *Hinc*II.

15 **Fig. 13.** Model for the transcriptional organization of SPI2 virulence genes. This model is based on the observation of the transcriptional direction of SPI2 genes, characterization of promoter activities

20 **Fig.14** shows the principle of how mutations having a different grade of attenuation can be generated. As shown in A, the inactivation of one effector gene such as *sse* results in a low grade of attenuation. As shown in B, the additional inactivation of a gene located outside the SPI2 locus such as *aroA* results in a medium grade of attenuation. By insertional mutation with a polar effect all genes in a polycistronic cluster are affected which results in a high grade of attenuation, as shown in C. As shown in D, the inactivation of a regulatory gene such as *ssrB* results in a supreme
25 attenuation.

30 **Fig.15** shows the principle of insertional mutation by example of insertional mutation into a virulence gene. Different cassettes such as SMC, GEC, TC and/or invertase cassette may be inserted into a cloned virulence gene, thus yielding an inactivated virulence gene which may be introduced into a cell by homologous recombination using a virulence gene cassette.

Fig.16 illustrates the selective marker cassette.

Fig.17 illustrates the gene expression cassette and the induction thereof in a two-phase system. The gene expression cassette comprises a promoter,
5 optionally a gene cassette comprising one or more expression units and optionally one or more transcriptional terminators for the expression units and/or a transcribed sequence 5' to the gene expression cassette.

Fig.18 shows the structural requirements of the gene expression unit for the
10 delivery of heterologous antigens into various compartments, i.e. accessory sequences that direct the targeting of the expression product.

Fig.19 shows a transactivator cassette in a one-phase system and a two-phase system.

Fig.20 shows different modes of gene expression as realized by the combination of different accessory sequences and/or cassettes in a one-phase system and a two-phase system.

Fig.21A shows the genomic sequence of a region of the SPI2 locus from
20 *Salmonella* comprising the complete sequences of the genes *ssaE* to *ssaI* and partial sequences of *ssaD* and *ssaJ* (cf. Fig.12).

Fig.21B shows the nucleotide sequence of a region of the SPI2 locus from
25 *Salmonella* comprising the coding sequences for *ssrA* and *ssrB*.

Figs.22A-Q each show the nucleotide sequence of the respective gene indicated.

Figs.23A-Q each show the amino acid sequence of the respective
30 polypeptide indicated.

Figs.24A,B each show a nucleotide sequence comprising an in vivo inducible promoter.

SEQUENCE LISTING

	SEQ ID NO: 1	genomic region	nucleic acid	FIG 21A
5	SEQ ID NO: 2	genomic region	nucleic acid	FIG 21B
	SEQ ID NO: 3	sseA	nucleic acid	FIG 22A
	SEQ ID NO: 4	sseA	translation product	FIG 23A
	SEQ ID NO: 5	sseB	nucleic acid	FIG 22B
	SEQ ID NO: 6	sseB	translation product	FIG 23B
10	SEQ ID NO: 7	sseC	nucleic acid	FIG 22C
	SEQ ID NO: 8	sseC	translation product	FIG 23C
	SEQ ID NO: 9	sseD	nucleic acid	FIG 22D
	SEQ ID NO: 10	sseD	translation product	
	SEQ ID NO: 11	sseD	protein	FIG 23D
15	SEQ ID NO: 12	sseE	nucleic acid	FIG 22E
	SEQ ID NO: 13	sseE	translation product	FIG 23E
	SEQ ID NO: 14	sseF	nucleic acid	FIG 22F
	SEQ ID NO: 15	sseF	translation product	FIG 23F
	SEQ ID NO: 16	sseG	nucleic acid	FIG 22G
20	SEQ ID NO: 17	sseG	translation product	FIG 23G
	SEQ ID NO: 18	sscA	nucleic acid	FIG 22H
	SEQ ID NO: 19	sscA	translation product	FIG 23H
	SEQ ID NO: 20	sscB	nucleic acid	FIG 22I
	SEQ ID NO: 21	sscB	translation product	FIG 23I
25	SEQ ID NO: 22	ssaD	nucleic acid	FIG 22J
	SEQ ID NO: 23	ssaD	translation product	FIG 23J
	SEQ ID NO: 24	ssaE	nucleic acid	FIG 22K
	SEQ ID NO: 25	ssaE	translation product	FIG 23K
	SEQ ID NO: 26	ssaG	nucleic acid	FIG 22L
30	SEQ ID NO: 27	ssaG	translation product	FIG 23L
	SEQ ID NO: 28	ssaH	nucleic acid	FIG 22M
	SEQ ID NO: 29	ssaH	translation product	FIG 23M
	SEQ ID NO: 30	ssaI	nucleic acid	FIG 22N
	SEQ ID NO: 31	ssaI	translation product	FIG 23N
35	SEQ ID NO: 32	ssaJ	nucleic acid	FIG 22O
	SEQ ID NO: 33	ssaJ	translation product	FIG 23O
	SEQ ID NO: 34	ssrA	nucleic acid	FIG 22P
	SEQ ID NO: 35	ssrA	translation product	FIG 23P
	SEQ ID NO: 36	ssrB	nucleic acid	FIG 22Q
40	SEQ ID NO: 37	ssrB	translation product	FIG 23Q
	SEQ ID NO: 38	Promoter A2	nucleic acid	FIG 24A
	SEQ ID NO: 39	Promoter B	nucleic acid	FIG 24B
	SEQ ID NO: 40	Esp A	protein	FIG 2A
	SEQ ID NO: 41	Esp D	protein	FIG 2B
45	SEQ ID NO: 42	Yop B	protein	FIG 2B
	SEQ ID NO: 43	Pep B	protein	FIG 2B
	SEQ ID NO: 44	D89	nucleic acid	page 33
	SEQ ID NO: 45	D90	nucleic acid	page 33

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	SEQ ID NO: 46	D91	nucleic acid	page 33
	SEQ ID NO: 47	D92	nucleic acid	page 33
	SEQ ID NO: 48	E25	nucleic acid	page 41
	SEQ ID NO: 49	E28	nucleic acid	page 41
5	SEQ ID NO: 50	E6	nucleic acid	page 42
	SEQ ID NO: 51	E4	nucleic acid	page 43
	SEQ ID NO: 52	sseC-del1	nucleic acid	page 44
	SEQ ID NO: 53	sseE-del1	nucleic acid	page 44
	SEQ ID NO: 54	sseC-For	nucleic acid	page 45
10	SEQ ID NO: 55	sseC-Rev	nucleic acid	page 45
	SEQ ID NO: 56	sseD-del1	nucleic acid	page 45
	SEQ ID NO: 57	sseD-del2	nucleic acid	page 45
	SEQ ID NO: 58	sseD-For	nucleic acid	page 46
	SEQ ID NO: 59	sseD-Rev	nucleic acid	page 46
15	SEQ ID NO: 60	sscB-del1	nucleic acid	page 47
	SEQ ID NO: 61	sscB-del2	nucleic acid	page 47
	SEQ ID NO: 62	sscB-For	nucleic acid	page 47
	SEQ ID NO: 63	sscB-Rev	nucleic acid	page 47/48
	SEQ ID NO: 64	ssrA-For	nucleic acid	page 66
20	SEQ ID NO: 65	ssrA-Rev	nucleic acid	page 66
	SEQ ID NO: 66	ssrB-For	nucleic acid	page 67
	SEQ ID NO: 67	ssrB-Rev	nucleic acid	page 67
	SEQ ID NO: 68	ssrA-del1	nucleic acid	page 67
	SEQ ID NO: 69	ssrB-del2	nucleic acid	page 68

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Claims

1. An isolated nucleic acid molecule, comprising a nucleic acid sequence
5 comprising at least 50 nucleotides
 - a) of the nucleic acid sequence of one of Figs. 21A, B,
 - b) of an allele of the nucleic acid sequence of one of Figs. 21A, B, or
 - c) of a nucleic acid sequence which under stringent conditions
10 hybridizes with the nucleic acid sequence of one of Figs. 21A, B.
2. The nucleic acid molecule according to claim 1, wherein said nucleic acid sequence comprises at least 50 nucleotides
 - 15 a) of the nucleic acid sequence of one of Figs. 22A - Q,
 - b) of a nucleic acid sequence, which corresponds to the nucleic acid sequence of one of Figs. 22A - Q within the degeneration of the genetic code, or
 - c) of a nucleic acid sequence which under stringent conditions
20 hybridizes with the nucleic acid sequence of one of Figs. 22A - Q.
3. The nucleic acid molecule according to claim 2, wherein said nucleic acid sequence comprises
 - a) the nucleic acid sequence of one of Figs. 22A - Q,
 - 25 b) a nucleic acid sequence, which corresponds to the nucleic acid sequence of one of Figs. 22A - Q within the degeneration of the genetic code, or

c) of a nucleic acid sequence which under stringent conditions hybridizes with the nucleic acid sequence of one of Figs. 22A - Q.

- 5 4. The nucleic acid molecule according to any one of the claims 1 to 3, wherein at least one coding region is functionally deleted.
- 10 5. The nucleic acid molecule according to any one of the claims 1 to 4, having inserted therein at least one insertion cassette for transposon or phage mediated insertion.
- 15 6. The nucleic acid molecule according to any one of the claims 1 to 5, wherein at least one heterologous nucleic acid molecule coding for a polypeptide or peptide is inserted or deletion-inserted.
- 20 7. The nucleic acid molecule according to claim 7, wherein the sequences flanking said heterologous nucleic acid molecule each have a length of at least 50 nucleotides, preferred 200 - 250 nucleotides.
- 20 8. The nucleic acid molecule according to claim 6 or 7, wherein said heterologous nucleic acid molecule comprises a nucleic acid sequence coding for a bacterial or viral antigen or homologue thereof.

9. The nucleic acid molecule according to claim 6 or 7, wherein said heterologous nucleic acid molecule comprises a nucleic acid sequence coding for a tumor antigen.
- 5 10. The nucleic acid molecule according to any one of the claims 7 to 9, wherein said heterologous nucleic acid molecule comprises at least one gene expression cassette.
- 10 11. The nucleic acid molecule according to any one of the claims 7 to 10, wherein said heterologous nucleic acid molecule comprises at least one transactivator cassette, selective marker cassette, invertase cassette or combination thereof.
- 15 12. The nucleic acid molecule according to any one of the claims 7 to 11, wherein said heterologous nucleic acid molecule comprises at least one nucleic acid sequence coding for a polypeptide or peptide targeting and/or immunostimulatory domain.
- 20 13. A recombinant vector comprising the nucleic acid molecule according to any one of the claims 1 to 12.
14. A cell comprising the nucleic acid molecule according to any one of the claims 5 to 12 or the recombinant vector according to claim 13.

15. The cell according to claim 14, wherein the cell is a gram-negative cell.
16. The cell according to claim 14, wherein the cell is a Salmonella cell.
- 5 17. A peptide or polypeptide comprising a peptide sequence comprising at least 20 amino acids
- a) of the sequence of Figs. 23A - Q, or
 - b) of a sequence which is 60 % homologous to the sequence of Figs. 23A - Q.
- 10
18. A polypeptide comprising the sequence
- a) of Figs. 23A - Q, or
 - b) which is 60 % homologous to the sequence of Figs. 23A-Q.
- 15 19. An antibody directed against the polypeptide according to any one of the claims 17 and 18.
- 20 20. A fusion protein comprising the polypeptide according to any one of the claims 17 and 18 having inserted or deletion-inserted or being fused C- or NH₂-terminally with at least one heterologous polypeptide.

21. The fusion protein according to claim 20, wherein the heterologous polypeptide is selected from bacterial, viral or tumor antigens.
22. An attenuated gram-negative cell comprising the SPI2 gene locus,
5 wherein at least one gene of the SPI2 locus is inactivated, wherein said inactivation results in an attenuation/reduction of virulence compared to the wild type of said cell.
23. The attenuated gram-negative cell according to claim 22, wherein at
10 least one inactivated gene is selected from effector (sse) genes, secretion apparatus (ssa) genes, chaperon (ssc) genes and regulation (ssr) genes.
24. The attenuated gram-negative cell according to claims 22 and 23,
15 wherein said cell is an Enterobacteriaceae cell, in particular, a Salmonella cell, a Shigella cell or a Vibrio cell.
25. The attenuated gram-negative cell according to claim 24, wherein said cell is a Salmonella cell.
- 20
26. The attenuated gram-negative cell according to claim 24 or 25, wherein said cell has a broad host range.

27. The attenuated gram-negative cell according to claim 26, wherein said cell is a Salmonella serotype Typhimurium Definitive Type 104 (DT104) cell.
- 5 28. The cell according to any one of the claims 22 to 27, wherein at least one inactivated gene is selected from sse, ssc and ssr.
29. The cell according to any one of the claims 22 to 28, wherein at least one inactivated gene comprises at least one sse gene.
- 10 30. The cell according to claim 29, wherein at least one sse gene is selected from sseC, sseD and sseE.
31. The cell according to any one of the claims 22 to 30, wherein at least one inactivated gene comprises at least one ssr gene.
- 15 32. The cell according to claim 31, wherein said at least one ssr gene is ssrB.
- 20 33. The cell according to any one of the claims 22 to 32, wherein at least one inactivated gene comprises at least one ssc gene.

34. The cell according to claim 33, wherein said at least one ssc gene is sscB.

5 35. The cell according to any one of the claims 22 to 34, wherein at least one gene is inactivated by a mutation comprising a deletion.

36. The cell according to claim 35, wherein said deletion comprises at least 6 nucleotides.

10 37. The cell according to any one of the claims 35 and 36, wherein the mutation comprises a deletion of the complete coding sequence for said gene.

15 38. The cell according to any one of the claims 22 to 37, wherein at least one gene is inactivated by a mutation comprising the insertion of a heterologous nucleic acid molecule.

39. The cell according to any one of the claims 35 to 38, wherein said mutation is a non-polar mutation.

20

40. The cell according to any one of the claims 22 to 39, wherein at least one additional gene located outside of the SPI2 locus is inactivated,

wherein the inactivation results in a further attenuation/reduction of virulence compared to the wild type.

5 41. The cell according to claim 40, wherein said additional gene comprises an aro gene.

42. The cell according to claim 41, wherein said aro gene is aro A.

10 43. The cell according to claim 40, wherein said additional gene is superoxide dismutase.

44. The cell according to any one of the claims 22 to 43, comprising at least one selective marker cassette.

15 45. The cell according to claim 44, wherein said selective marker cassette is capable of conferring an antibiotic resistance to the cell.

46. The cell according to any one of the claims 22 to 45 comprising at least one gene expression cassette.

47. The cell according to any one of the claims 22 to 46 comprising at least one transactivator cassette.
48. The cell according to any one of the claims 22 to 47 comprising at least one invertase cassette.
49. The cell according to any one of the claims 22 to 48 comprising at least one insertion cassette.
50. A carrier for the presentation of an antigen to a host, which carrier is an attenuated gram-negative cell according to any one of the claims 22 to 49, wherein said cell comprises at least one heterologous nucleic acid molecule comprising a nucleic acid sequence coding for said antigen, wherein said cell is capable of expressing said nucleic acid molecule or capable of causing the expression of said nucleic acid molecule in a target cell.
51. The carrier according to claim 50, wherein said nucleic acid molecule comprises a nucleic acid sequence coding for a bacterial or viral antigen or a tumor antigen.
52. The carrier according to claim 51, wherein said nucleic acid sequence codes for an antigen from *Helicobacter pylori*, *Chlamydia pneumoniae*,

Borrelia burgdorferi, *Nanobacteria*, Hepatitis virus, human papilloma virus or Herpes virus.

5 53. The carrier according to any of the claims 50 to 52, wherein said nucleic acid molecule is inserted into the SPI2 locus.

54. The carrier according to claim 53, wherein said nucleic acid molecule is inserted into an *sse* gene.

10 55. The carrier according to claim 54, wherein said *sse* gene is selected from *sseC*, *sseD* and *sseE*.

56. The carrier according to any one of the claims 50 to 55, wherein said insertion is a non-polar insertion.

15

57. The carrier according to any one of the claims 50 to 56, wherein the expression of said heterologous nucleic acid molecule is tissue specific.

20 58. The carrier according to any one of the claims 50 to 57, wherein the expression of said heterologous nucleic acid is inducible.

59. The carrier according to any one of the claims 50 to 58, wherein the expression of said heterologous nucleic acid is activated in a target cell.
- 5 60. The carrier according to claim 59, wherein said target cell is a macrophage.
61. The carrier according to any of the claims 50 to 60, wherein said nucleic acid molecule comprises a nucleic acid sequence coding for a
10 least one polypeptide or peptide targeting and/or immunostimulatory domain.
62. The carrier according to any one of the claims 50 to 60, wherein said nucleic acid molecule codes for a fusion protein.
- 15 63. The cell according to any one of the claims 50 to 62, wherein the expression product of said nucleic acid molecule remains in the cytosole of said carrier.
- 20 64. The carrier according to any one of the claims 50 to 62, wherein the expression product of said nucleic acid molecule is directed to the periplasmatic space of said carrier.

65. The carrier according to any one of the claims 50 to 62, wherein the expression product of said nucleic acid molecule is directed to the outer membrane of said carrier.
- 5 66. The carrier according to any one of the claims 50 to 62, wherein the expression product of said nucleic acid molecule is secreted.
67. The carrier according to claim 66, wherein the expression product of said nucleic acid molecule is secreted by the type III secretion system.
- 10 68. The carrier according to claim 67, wherein the expression product of said nucleic acid molecule is secreted by the SPI2 type III secretion system.
- 15 69. An attenuated gram-negative cell comprising the SPI2 gene locus, characterized by a lack of at least one SPI2 polypeptide, wherein said lack results in an attenuation/reduction of virulence compared to the wild type of said cell.
- 20 70. The attenuated gram-negative cell according to claim 69, wherein said missing polypeptide is selected from effector (sse) polypeptides, secretion apparatus (ssa) polypeptides, chaperon (ssc) polypeptides and regulatory (ssr) polypeptides.

71. A carrier for the presentation of an antigen to a host, which carrier is an attenuated gram-negative cell according to claims 69 or 70, further characterized by the presence of at least one heterologous peptide or polypeptide having immunogenic properties.

5

72. A pharmaceutical composition, comprising as an active agent an immunologically protective living vaccine, which is an attenuated cell according to any one of the claims 22 to 49, 69 and 70 or a carrier according to any one of the claims 50 to 68 and 71.

10

73. The composition according to claim 72 together with pharmaceutically acceptable diluents, carriers and/or adjuvants.

15

74. The composition according to any one of the claims 72 and 73, which is suitable for administration to a mucosal surface or via the parenteral route.

20

75. A method for the preparation of a living vaccine, comprising providing a living gram-negative cell comprising the SPI2 locus and inactivating at least one gene of the SPI2 locus to obtain an attenuated gram-negative cell according to any one of the claims 22 to 49, 69 and 70.

76. The method of claim 75, further comprising inserting at least one heterologous nucleic acid molecule coding for an antigen to obtain a carrier according to any one of the claims 50 to 68 and 71.
- 5 77. A method for the preparation of a living vaccine composition comprising formulating an attenuated cell according to any one of the claims 22 to 49, 69 and 70 or a carrier according to any one of the claims 50 to 68 and 71 in a pharmaceutically effective amount together with pharmaceutically acceptable diluents, carriers and/or
10 adjuvants.
78. A method for the detection of an attenuated cell according to any one of the claims 22 to 49, 69 and 70 or a carrier according to any one of the claims 50 to 68 and 71, comprising providing a sample containing
15 said cell and detecting a specific property not present in wild type.
79. A method for establishing a library of attenuated gram-negative cells comprising obtaining at least two attenuated gram-negative cells according to any one of the claims 22 to 49, 69 and 70, determining
20 the pathogenicities of said cells, and determining the relation of the pathogenicities of said cells.
80. The method according to claim 79 further comprising determining the immunogenicities of said cells and determining the relation of the
25 immunogenicities of said cells.

81. The method of claim 80, wherein the determination of the immunogenicity is a determination of the humoral, cellular and/or mucosal immunogenicity.

5 82. A method for establishing a library of attenuated carriers for the presentation of an antigen to a host, comprising obtaining at least two carriers according to any one the claims 50 to 68 and 71, determining (a) the pathogenicities of said cells and the relation of the pathogenicities of said cells, and (b) determining the effect of said
10 antigen presentation in said host and determining the relation of said effects caused by said cells.

83. The method of claim 82, wherein the effect of antigen presentation is determined at humoral, cellular and/or mucosal level.

15

84. The method according to claim 82 or 83 further comprising determining the immunogenicities of said cells and determining the relation of the immunogenicities of said cells, wherein said determination optionally is a determination of the humoral, cellular
20 and/or mucosal immunogenicity.

85. The use of an attenuated cell according to any one of the claims 22 to 49, 69 and 70 or a carrier according to any one of the claims 50 to 68 and 71 for the preparation of a drug for the preventive or therapeutic

treatment of an acute or chronic disease caused essentially by a bacterium or virus.

- 5 86. The use according to claim 85, wherein said disease is caused essentially by a Salmonella cell.
87. The use of a carrier according to any one of the claims 50 to 68 and 71 for the preparation of a drug for the preventive or therapeutic treatment of a tumour.
- 10 88. The use of a nucleic acid molecule according to any one of the claims 1 to 12 or a vector according to claim 13 for the preparation of an attenuated cell, a living vaccine or a carrier for the presentation of an antigen to a host.
- 15 89. Use of the Salmonella SPI2 locus for the preparation of an attenuated cell, a living vaccine or a carrier for the presentation of an antigen to a host.
- 20 90. Use of a virulence gene locus of a gram-negative cell for the preparation of a carrier for the presentation of an antigen to a host.

91. An isolated nucleic acid molecule comprising a nucleic acid of at least 100 nucleotides

a) of the nucleic acid sequence of one of Figs.24A, B

b) of a nucleic acid sequence which under stringent conditions hybridizes with the nucleic acid sequence of one of Figs.24A, B.

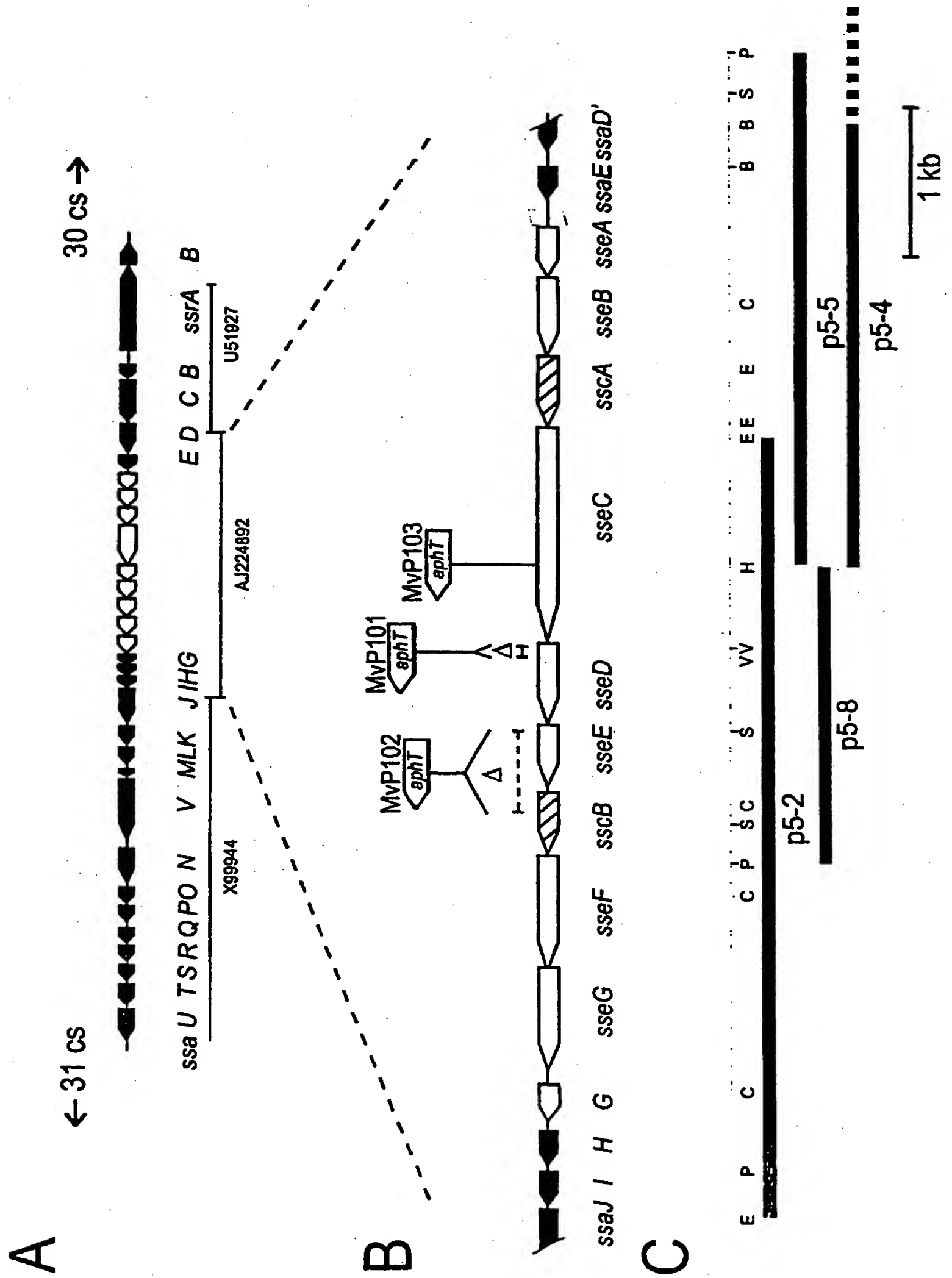
92. The nucleic acid molecule according to claim 91, wherein said nucleic acid molecule is capable of inducing the expression of a nucleic acid sequence coding for a peptide or polypeptide operatively linked to said nucleic acid molecule.

93. Expression system for the in-vivo inducible expression of a heterologous nucleic acid in a target cell, comprising a carrier cell for said heterologous nucleic acid, wherein said carrier cell comprises (a) a polypeptide having the amino acid sequence shown in Figure 23P (ssrA) or a functional homologue thereof, (b) a polypeptide having the amino acid sequence shown in Figure 23Q (ssrB) or a functional homologue thereof, and (c) the nucleic acid molecule according to claim 92.

94. Expression system according to claim 91, wherein said target cell is a macrophage.

95. Expression system according to claims 93 and 94, wherein said carrier cell is a *Salmonella* cell.
96. The expression system according to any of the claims 93 to 95,
5 wherein said target cell comprises a gene expression cassette.
97. The expression system according to any of the claims 93 to 96, wherein said target cell comprises an insertion cassette.
- 10 98. The expression system according to any of the claims 93 to 97, wherein said target cell comprises a heterologous nucleic acid molecule coding for a peptide or polypeptide.
- 15 99. Use of the nucleic acid molecule according to claim 92 for the in vivo inducible expression of a heterologous nucleic acid molecule.
100. Use of the nucleic acid molecule according to claim 92 for the detection of in vivo inducible promoters.

Fig. 1: position of mutations in MvP101, MvP102 and MvP103



Alignment of SseB to EspA

SseB	I M S G N - I L W G S Q N P I V F K N . . . S F G V S N A D T G S Q D D L S Q Q N P F A E G Y G V L 46
EspA	I M D T S T T A S V A S A N A S T S T S M A Y D L G S M S K D D - V I D L F N K L G V F Q A A I L M F 49
SseB	47 L I L M V I Q A I A N N K F I E V Q K N A E R A R N T Q E K S N E M D E V I A K A A K G - D A K T 95
EspA	50 A Y M Y Q A Q S D L S I A K F A D M N E A S K E S T T A Q K M A N L V D A K I A D V Q S S S D K N A 99
SseB	96 K E E V P E D V I K Y M R D - - N G I L I D G M T I D D Y M A K Y G D H G K L D K G G L Q A I K A A 143
EspA	100 K A Q L P D E V I S Y I N D P R N D I T I S G - - I D N I N A Q L G A G D L Q T V K A A 141
SseB	144 L D N D A N R N T D L M S Q G Q I T I Q K M S Q E L N A V L T Q L T G L I S K W G E I S S M I A Q K 193
EspA	142 I S A K A N N L T T T V N N S Q L E I Q Q M S N T L N L L T S A R S D M Q S L Q Y R T I S G I S L G 191
SseB	194 T Y S 196
EspA	192 K 192

Fig. 2a

Alignment of SseC to EspD, YopB and PepB

SseC	1	M	N	R	I	H	S	N	S	D	S	A	A	G	-	-	V	T	A	L	T	H	H	H	L	S	N	V	S	C	V	S	S	G	S	L	G	K	R	Q	H	R	V	N	S	T	F	G	D	G	N	A	C	L	L	S	G	K	-	-	56			
EspD	1	M	L	N	V	N	N	D	I	Q	S	V	R	S	G	A	S	A	A	T	A	T	S	G	I	N	Q	S	E	V	T	S	A	L	D	L	Q	L	V	K	S	T	A	P	S	A	S	W	T	E	S	T	A	L	A	T	P	P	A	G	H	60		
YopB	1	M	S	A	L	I	T	H	D	R	S	T	P	-	-	-	V	T	G	S	L	V	P	Y	I	E	T	P	A	P	L	Q	T	Q	V	A	G	E	L	K	D	K	N	G	G	V	S	S	Q	G	V	Q	L	P	A	P	-	-	55					
PepB	1	M	N	P	I	T	L	E	R	A	G	L	P	Y	G	V	A	D	A	G	D	I	P	A	L	G	R	P	V	A	R	D	V	E	S	L	R	V	E	R	L	A	A	P	A	A	S	A	S	G	T	G	V	A	L	T	P	P	-	-	58			
SseC	57	-	-	-	-	-	I	S	L	Q	E	A	S	N	A	L	K	Q	-	-	-	-	-	-	-	L	L	D	A	V	P	G	N	H	K	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	96				
EspD	61	S	L	V	T	P	S	A	A	E	D	V	L	S	K	L	F	G	G	I	S	G	E	V	T	S	R	T	E	G	T	E	P	Q	R	S	T	Q	N	A	S	S	G	Y	P	Y	L	S	Q	V	N	N	V	D	P	Q	A	M	M	120				
YopB	56	-	-	-	-	-	L	A	V	V	A	S	Q	V	T	E	G	Q	Q	E	I	T	K	L	L	E	S	V	T	R	G	T	A	G	S	-	-	-	Q	L	I	S	N	Y	V	S	V	L	T	N	F	T	L	A	S	P	D	T	F	E	I	E	109	
PepB	59	-	-	-	-	-	S	A	A	S	Q	Q	R	L	E	V	A	N	R	A	E	I	A	S	L	V	Q	A	V	G	E	D	A	G	L	A	R	-	-	Q	V	V	L	A	G	A	S	T	L	L	S	A	G	L	M	S	P	Q	A	F	E	I	E	113
SseC	97	M	T	S	L	I	L	N	V	F	G	N	A	Q	S	L	C	Q	Q	L	E	R	A	T	E	V	Q	N	A	L	R	N	K	Q	V	K	E	V	Q	E	Q	I	Q	K	A	I	E	Q	E	D	K	A	R	K	A	G	I	F	G	A	156			
EspD	121	A	T	L	L	S	L	D	A	S	A	Q	R	V	A	S	M	K	N	S	N	E	I	Y	A	D	G	Q	N	K	A	L	D	N	K	T	L	E	F	K	Q	L	E	Q	K	A	E	E	K	A	Q	K	S	K	I	I	V	G	Q	180				
YopB	110	L	G	K	L	V	S	N	L	E	E	V	R	K	D	I	K	I	A	D	T	Q	R	L	H	E	-	Q	N	-	-	M	K	K	I	E	E	N	Q	E	K	I	K	E	T	E	E	N	A	K	Q	V	K	K	S	G	M	A	S	K	165			
PepB	114	L	A	K	I	T	G	E	V	E	N	Q	K	K	L	K	L	T	E	I	E	Q	A	R	K	-	Q	N	-	-	L	Q	K	M	E	D	N	Q	K	I	R	E	S	E	E	A	A	K	E	A	Q	K	S	G	L	A	A	K	169					
SseC	157	I	F	D	W	I	T	G	I	F	E	T	V	T	G	A	L	K	V	I	E	G	F	L	S	G	N	P	A	E	M	A	S	G	V	A	Y	M	A	A	G	C	A	G	M	V	K	A	G	A	E	T	A	M	M	C	G	A	D	H	D	216		
EspD	181	V	F	G	W	L	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	223				
YopB	166	I	F	G	W	L	I	A	I	A	S	V	V	I	G	A	I	M	V	A	S	G	V	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	216				
PepB	170	I	F	G	W	I	S	A	I	A	S	I	I	V	G	A	I	M	V	A	T	G	V	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	220				
SseC	217	T	C	Q	A	I	I	D	V	T	S	K	I	Q	F	G	C	E	A	V	A	L	A	L	D	V	F	Q	I	G	R	A	F	M	A	T	R	G	L	S	G	A	A	K	V	L	D	S	G	F	G	E	E	V	V	E	R	M	V	G	276			
EspD	224	-	A	P	Q	A	L	K	T	A	A	Q	A	F	G	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	276				
YopB	217	I	S	Q	E	A	M	Q	V	L	G	P	I	L	T	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	270				
PepB	221	I	S	K	E	V	M	E	K	L	G	P	A	L	M	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	274				
SseC	277	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	319				
EspD	277	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	308				
YopB	271	G	A	E	F	S	A	K	V	A	Q	I	S	T	G	I	S	N	T	V	G	S	A	V	T	K	L	G	G	S	F	G	S	L	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	316				
PepB	275	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	305				
SseC	320	E	F	S	R	N	V	E	N	N	M	T	R	S	A	G	K	S	F	T	K	E	G	V	K	A	M	A	K	E	A	A	K	E	A	L	E	K	C	V	Q	E	G	G	K	F	L	K	K	F	R	N	K	V	L	F	N	M	F	K	379			
EspD	309	N	N	D	A	A	Y	Y	N	V	L	S	Q	V	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	356					
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PepB	306	D	L	T	L	D	V	A	N	G	A	Q	A	T	H	S	G	F	Q	A	K	A	A	N	R	Q	A	D	V	Q	E	S	R	A	D	L	T	T	L	Q	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	357
SseC	380	K	I	L	Y	A	L	L	R	D	C	S	F	K	G	L	Q	A	I	R	C	A	T	E	G	A	S	Q	M	N	T	G	M	V	N	T	E	K	A	K	I	E	K	K	I	E	Q	L	I	T	Q	Q	R	F	L	D	F	435						
EspD	357	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	380				
YopB	369	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	401				
PepB	358	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	390				

Fig. 2b

Fig. 3

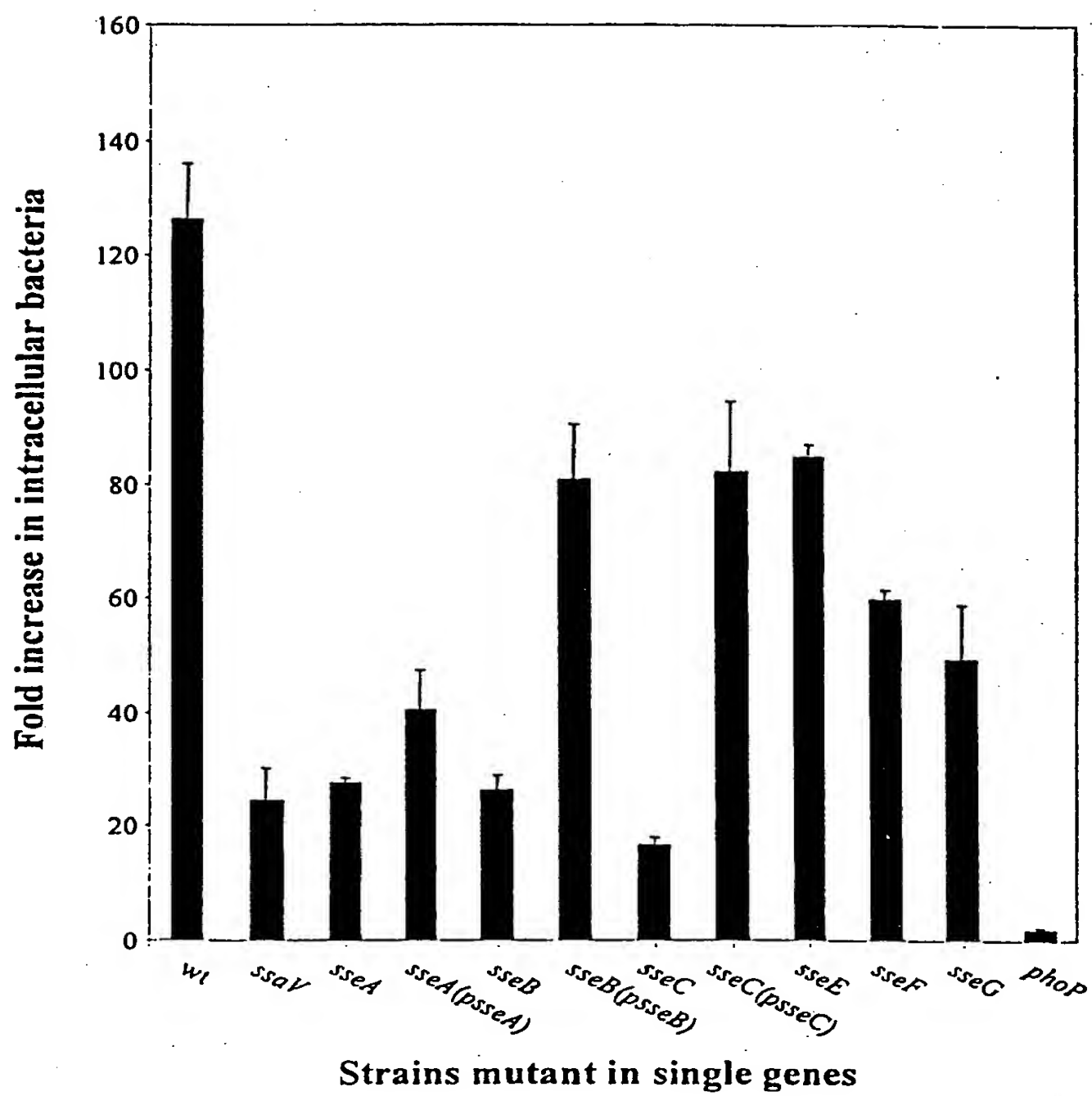


Fig. 4A

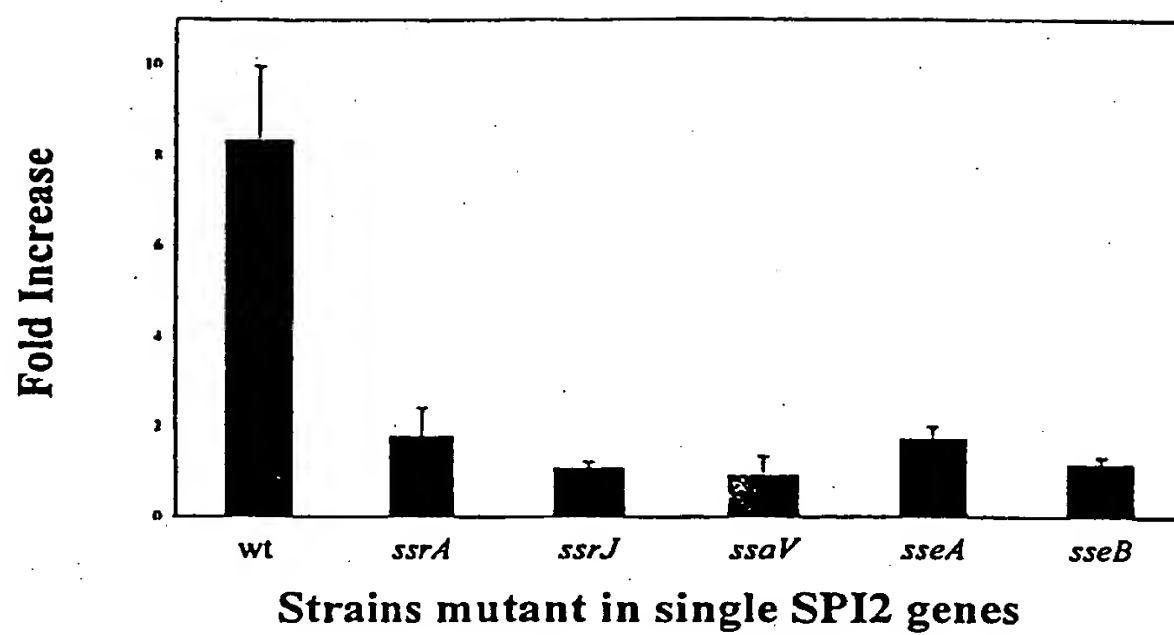
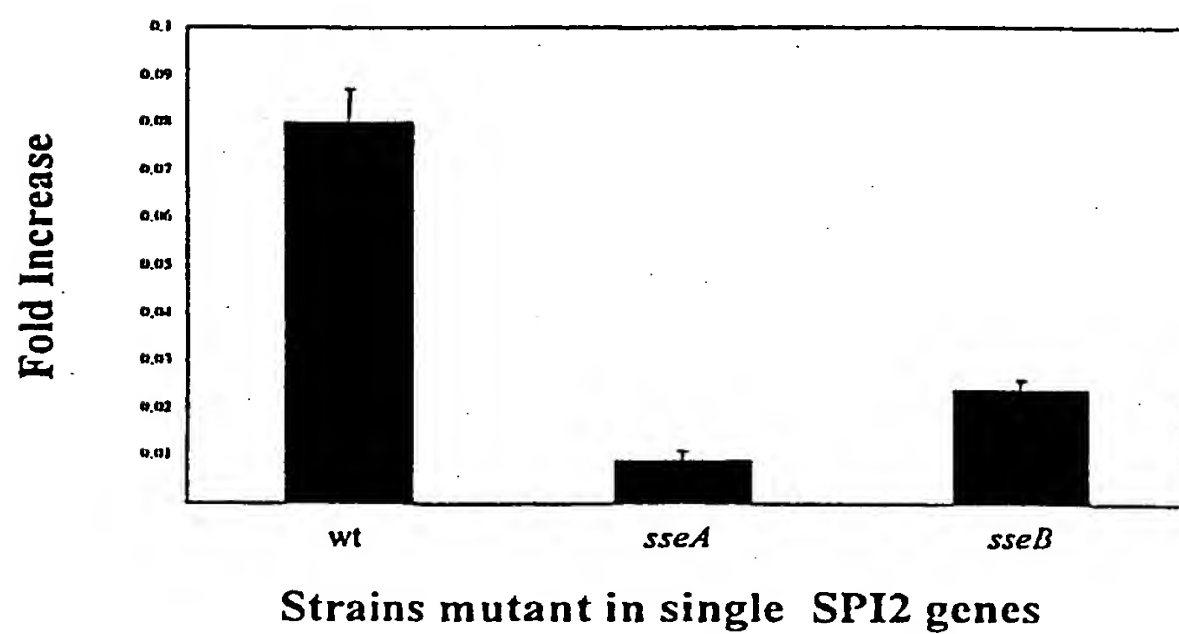


Fig. 4B



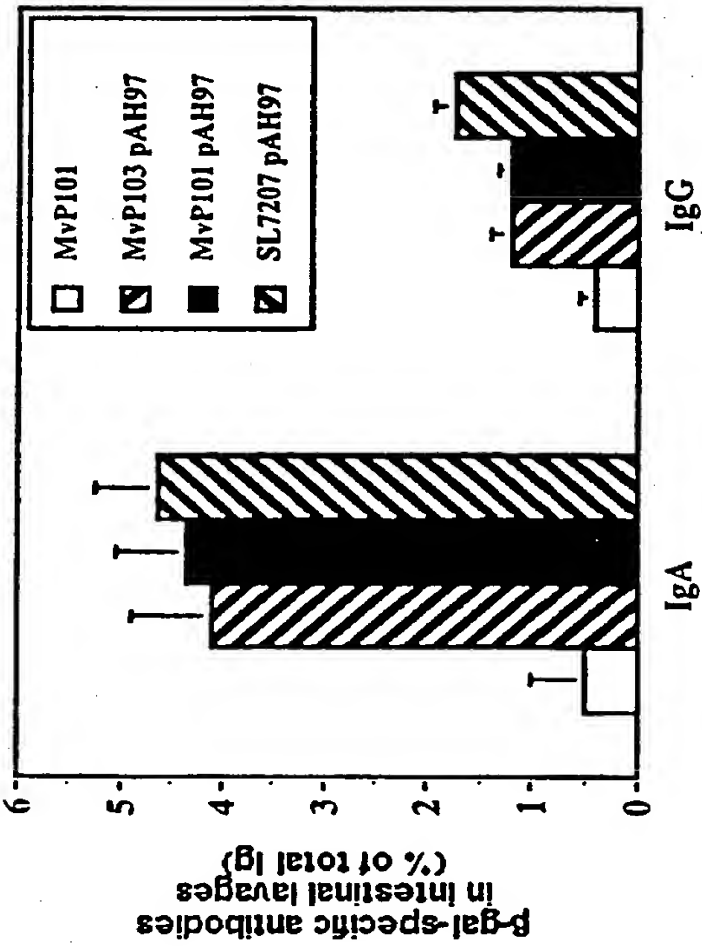


Fig. 5

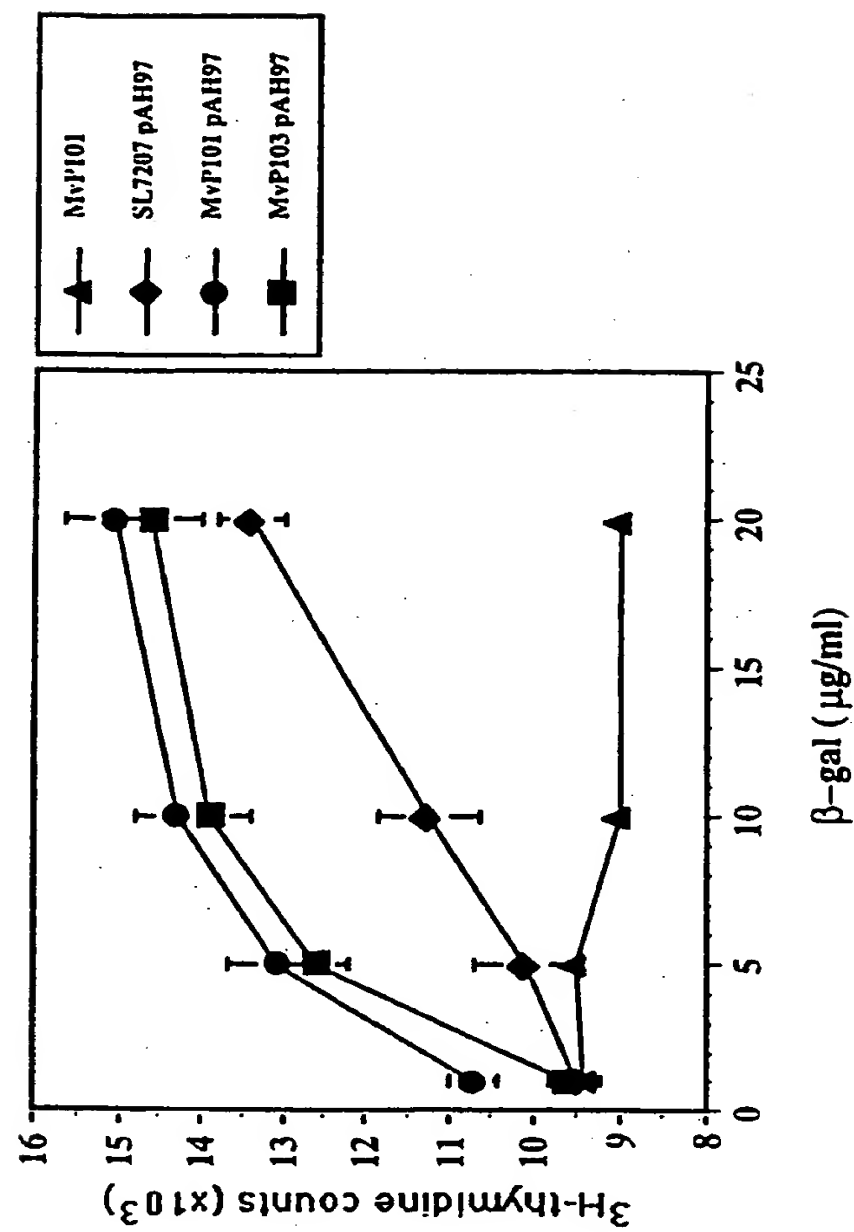


Fig. 6

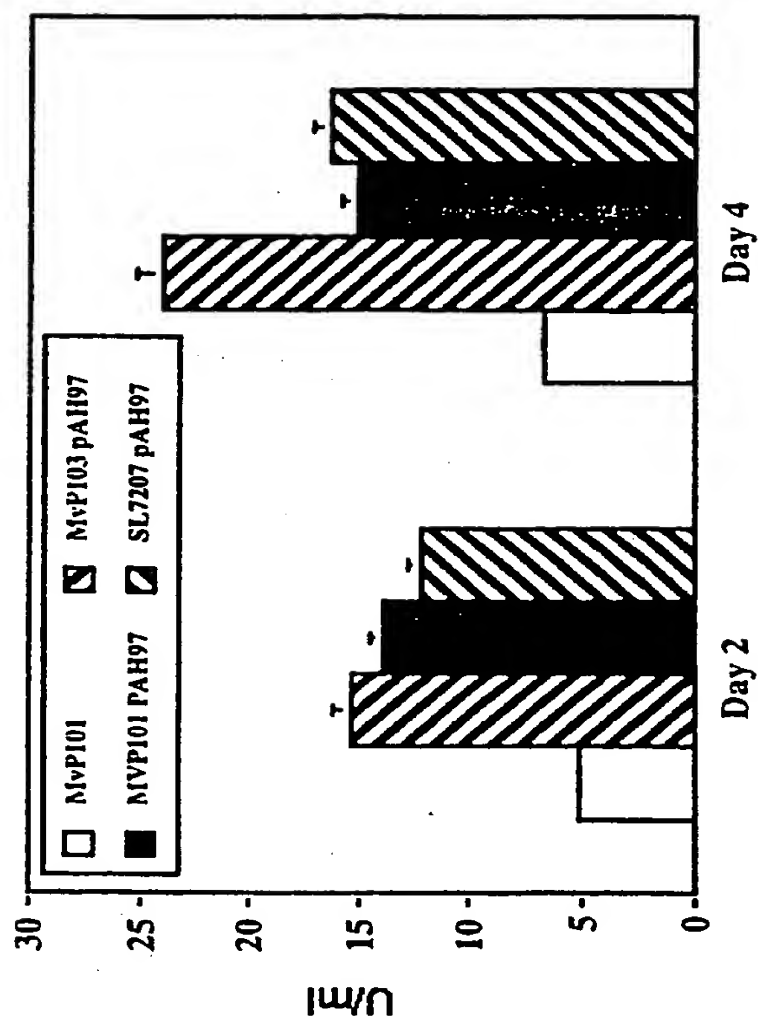


Fig. 7

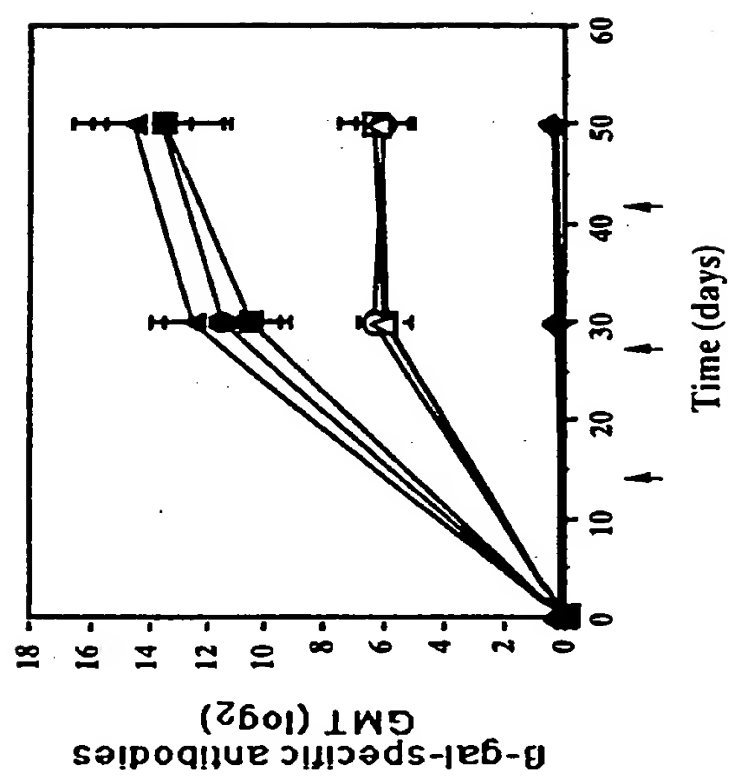


Fig. 8

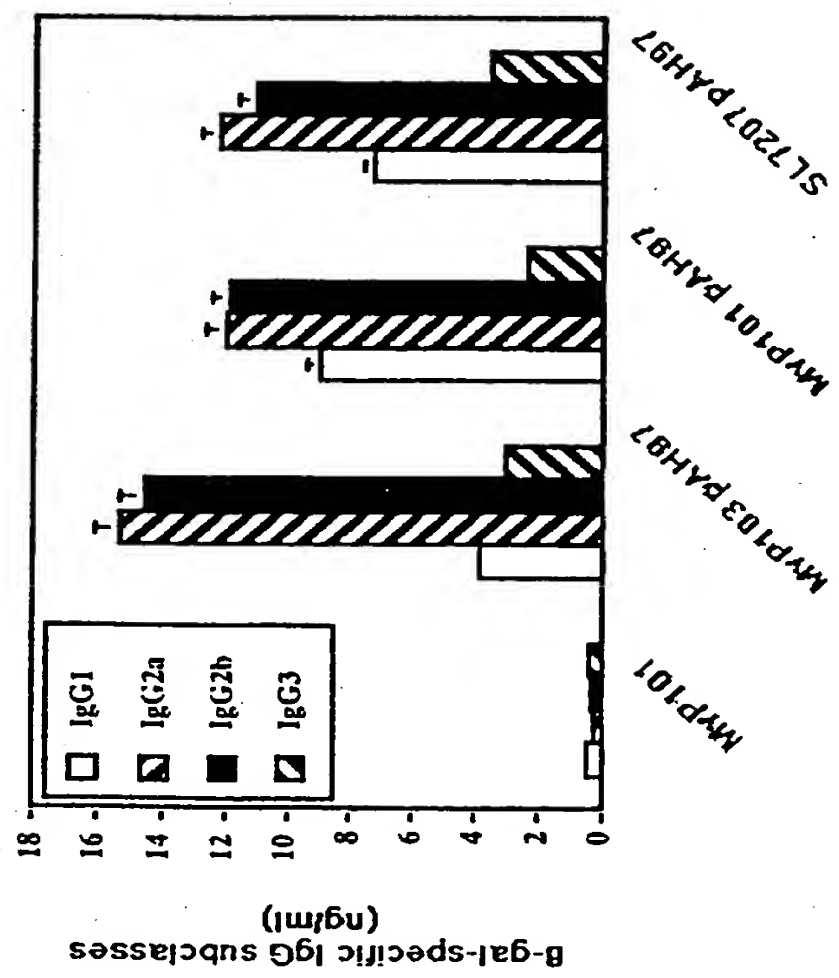


Fig. 9

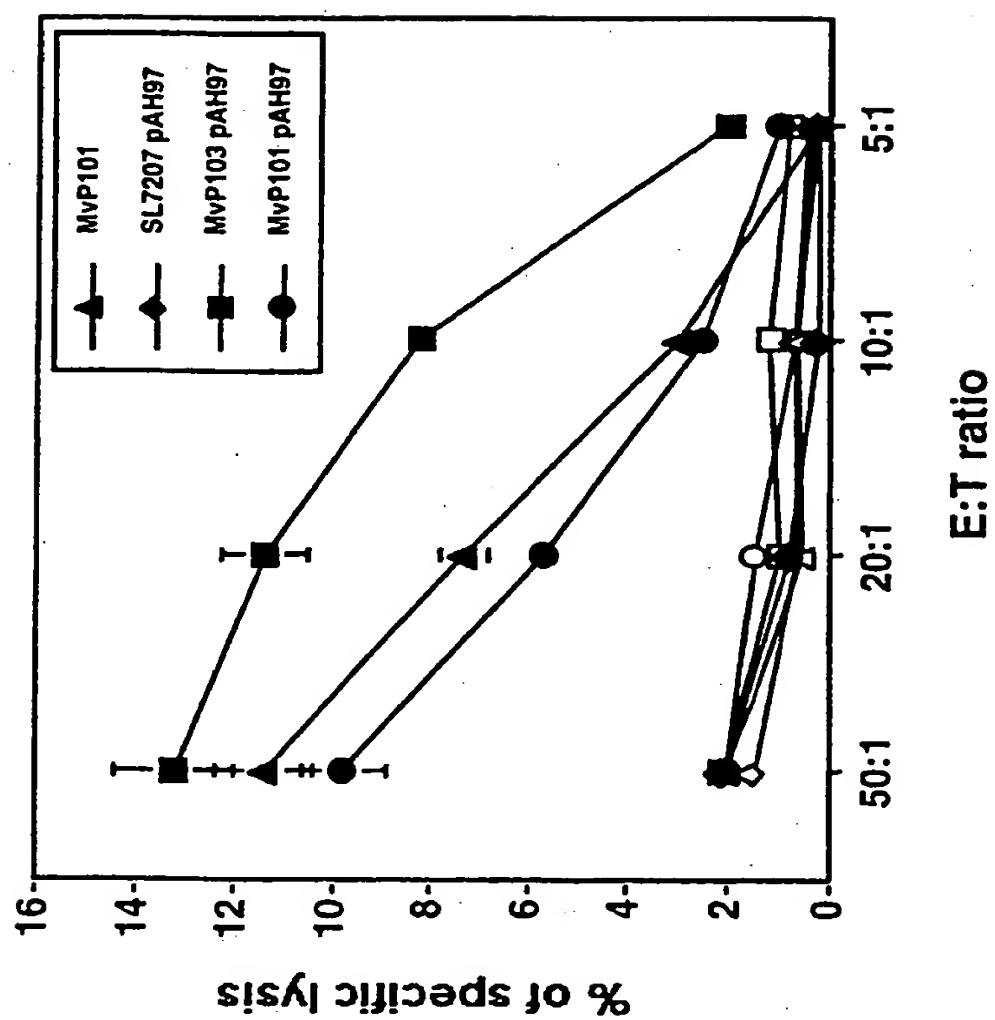


Fig. 10

Fig. 11

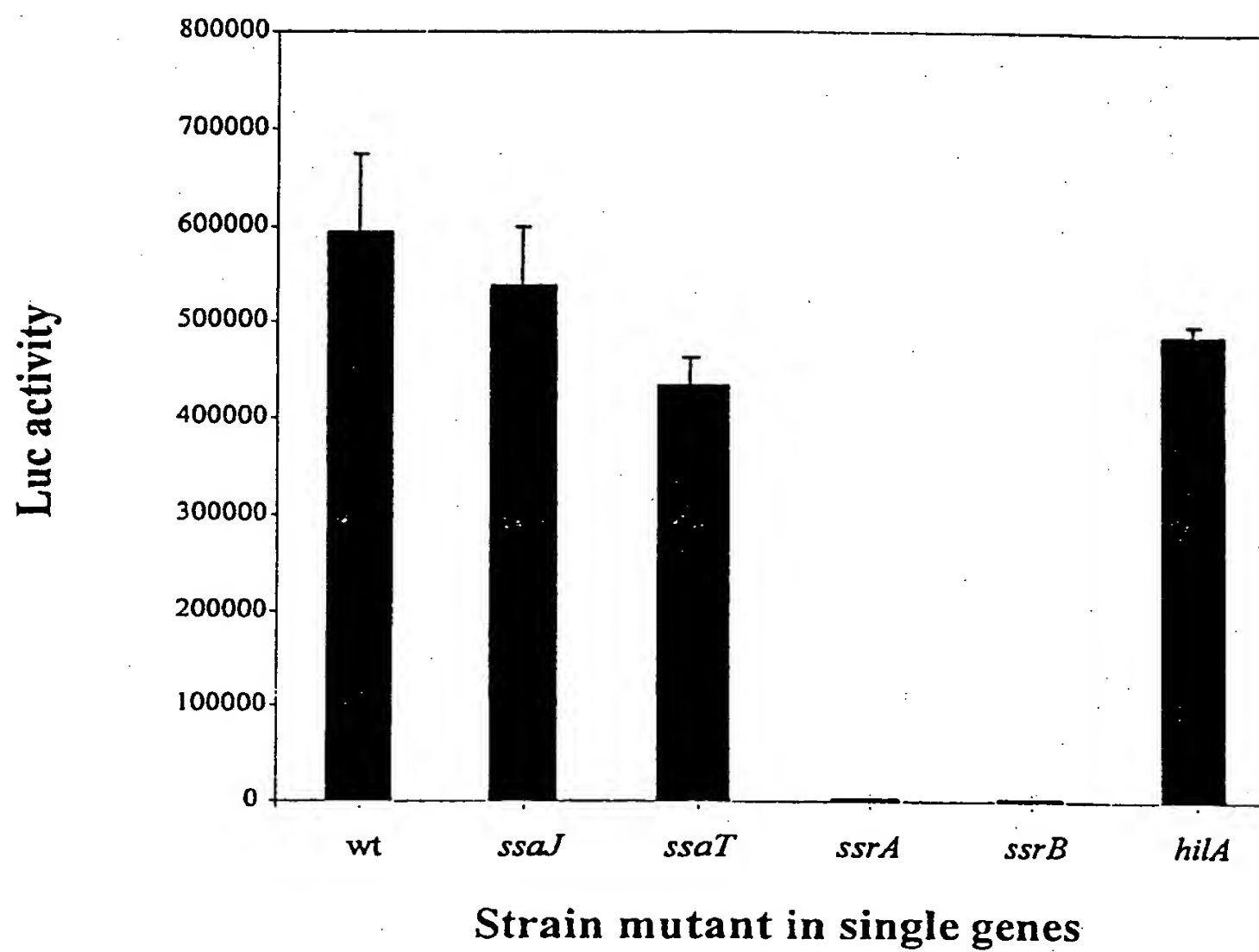


Fig.12: position of mutations in MvP284 and MvP320

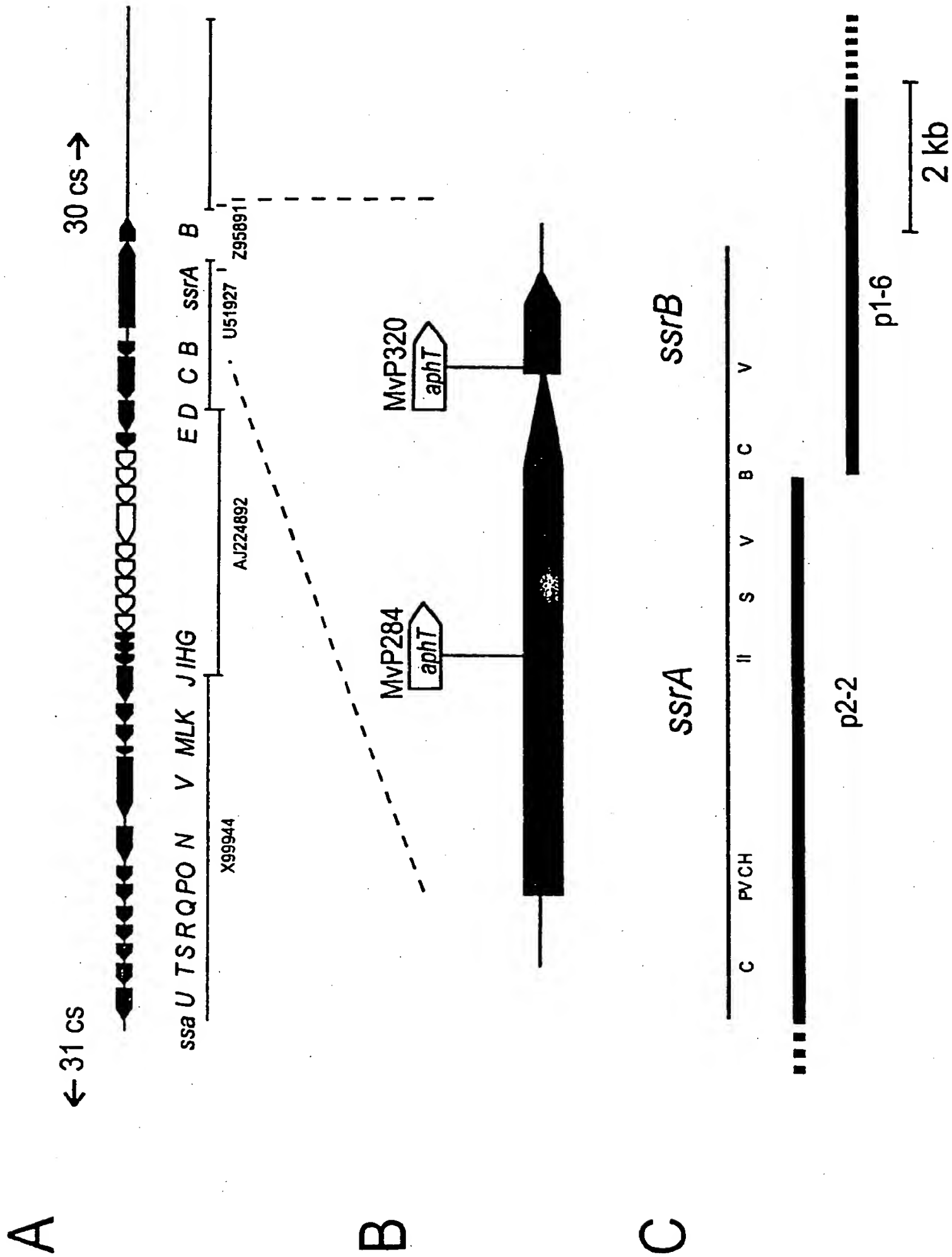
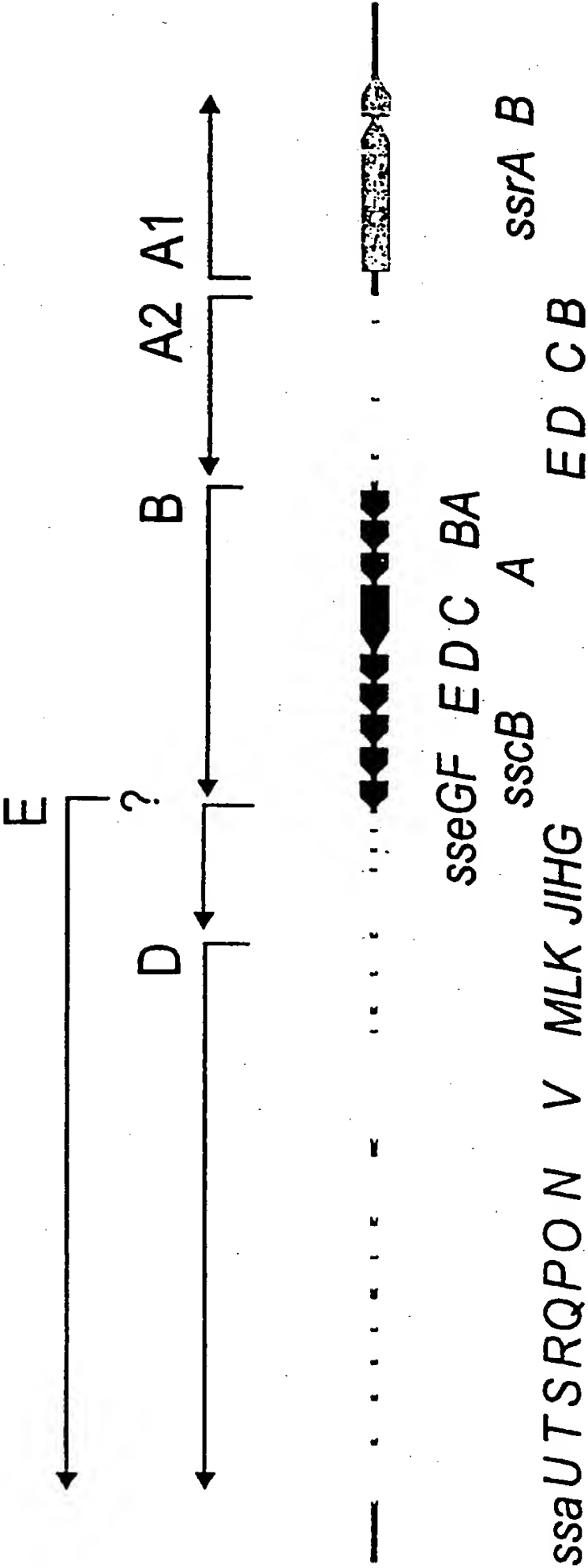
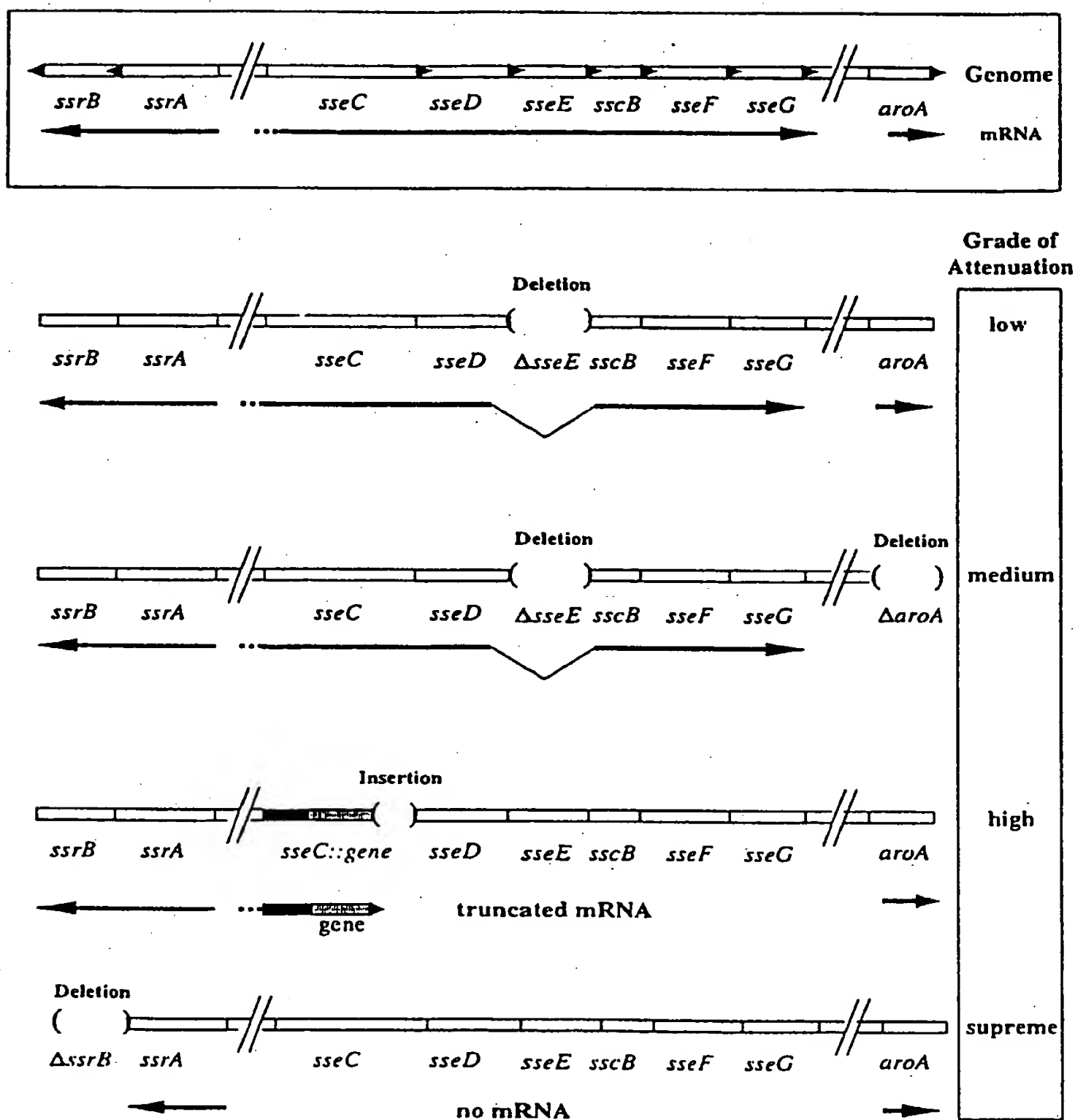


Fig./3: model for the transcriptional units for SP12 virulence genes



Principle of Attenuation

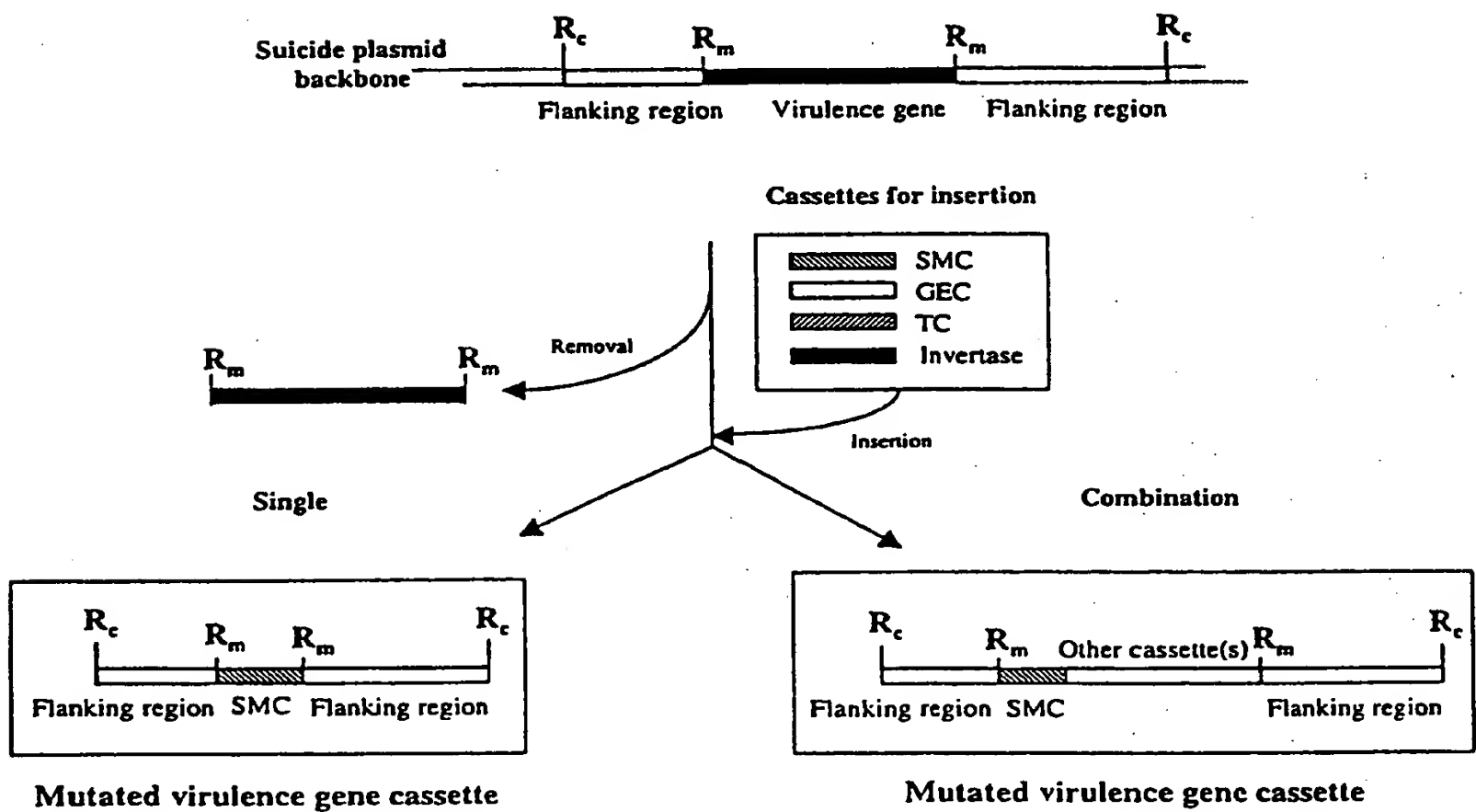
Schematic Instruction for the Generation of Different Mutations with Increasing Grade of Attenuation



Principle of insertional mutation

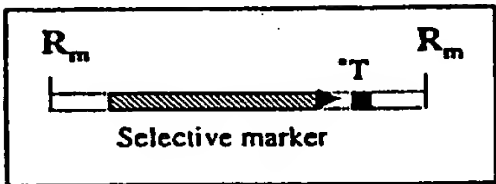
R_c = Restriction sites for cloning of virulence gene cluster fragment

R_m = Restriction sites for gene mutation



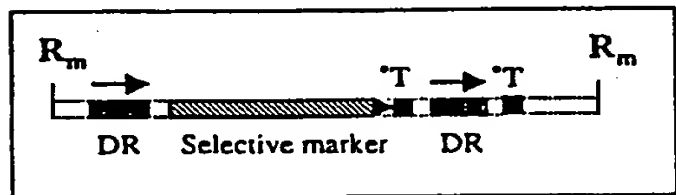
Selective Marker Cassette (SMC)

Permanent selective marker cassette



*T = Optional transcriptional terminator if polar insertional mutation is required

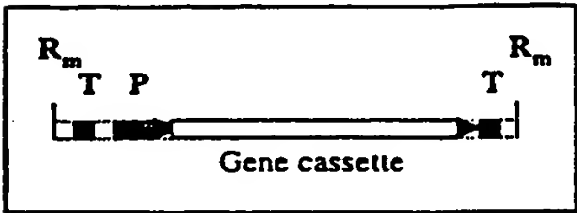
Revertible selective marker cassette



DR= direct repeat

Gene Expression Cassette (GEC)

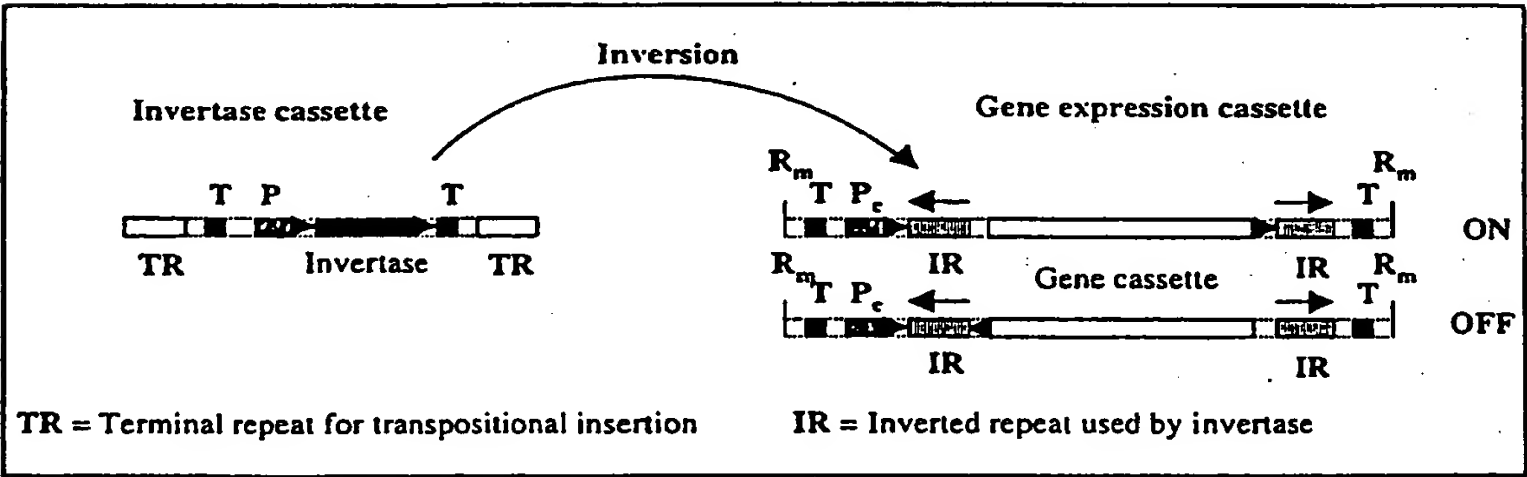
One Phase System



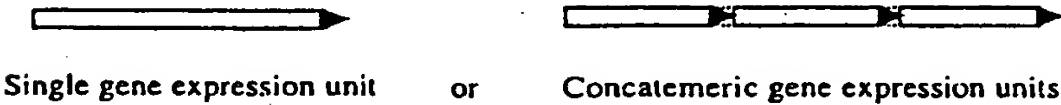
P = Promoter consisting of either a
- promoter acting constitutively in *Salmonella*
- a *Salmonella in vivo* inducible promoter or
- an other promoter

T = Transcriptional terminator

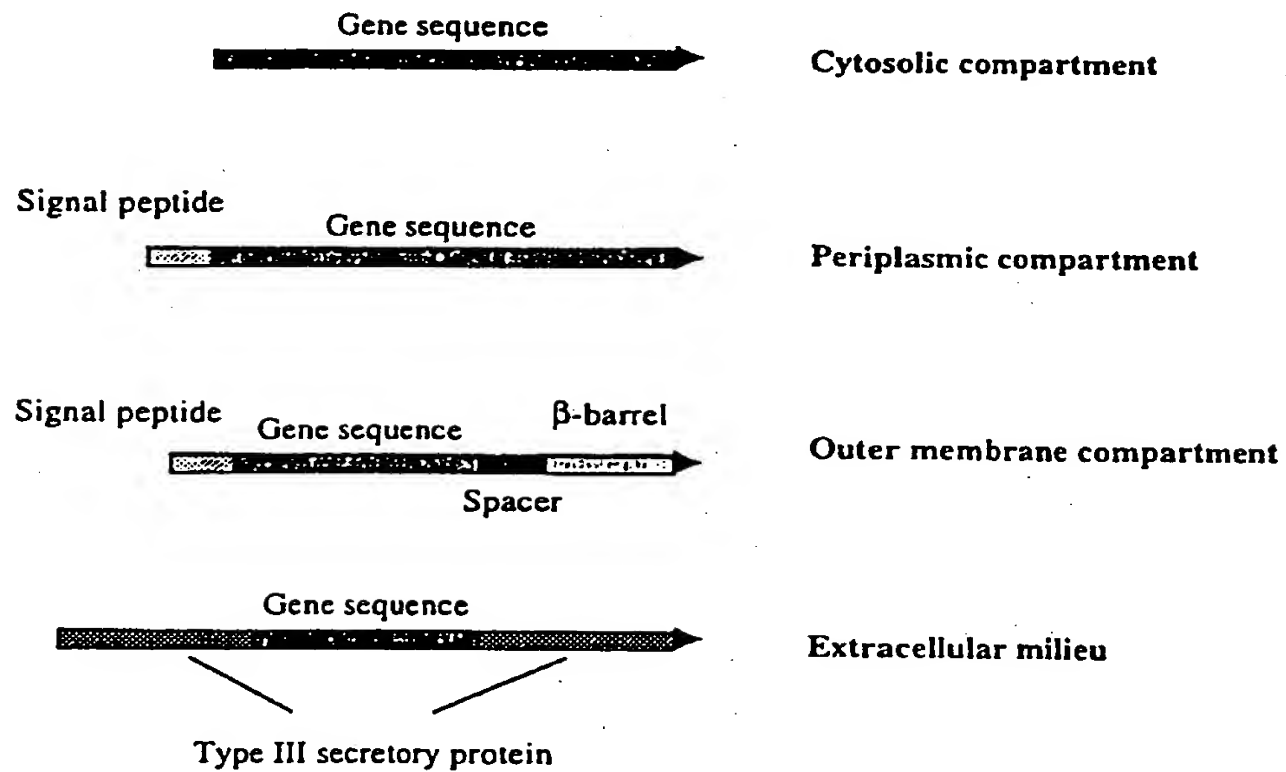
Two Phase System



Gene cassette:



Structural requirements of the gene expression unit for the delivery of heterologous antigens into the various *Salmonella* compartments



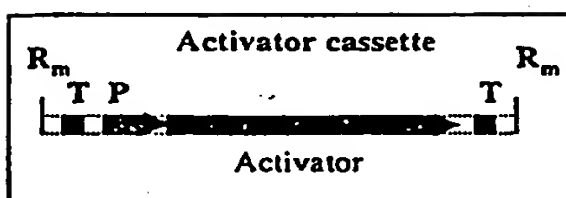
Transactivator Cassette (TC)

P = Promoter consisting of either a

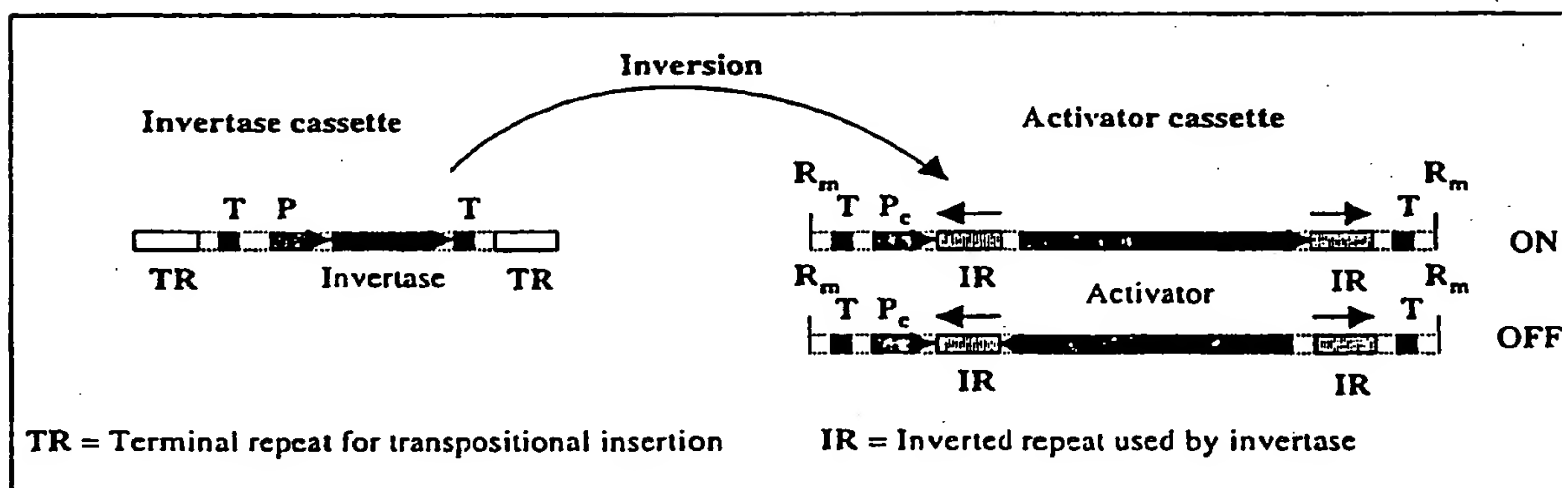
- promoter acting constitutively in *Salmonella*
- a *Salmonella in vivo* inducible promoter or
- an other promoter

P_c = Constitutive promoter

One Phase System



Two Phase System



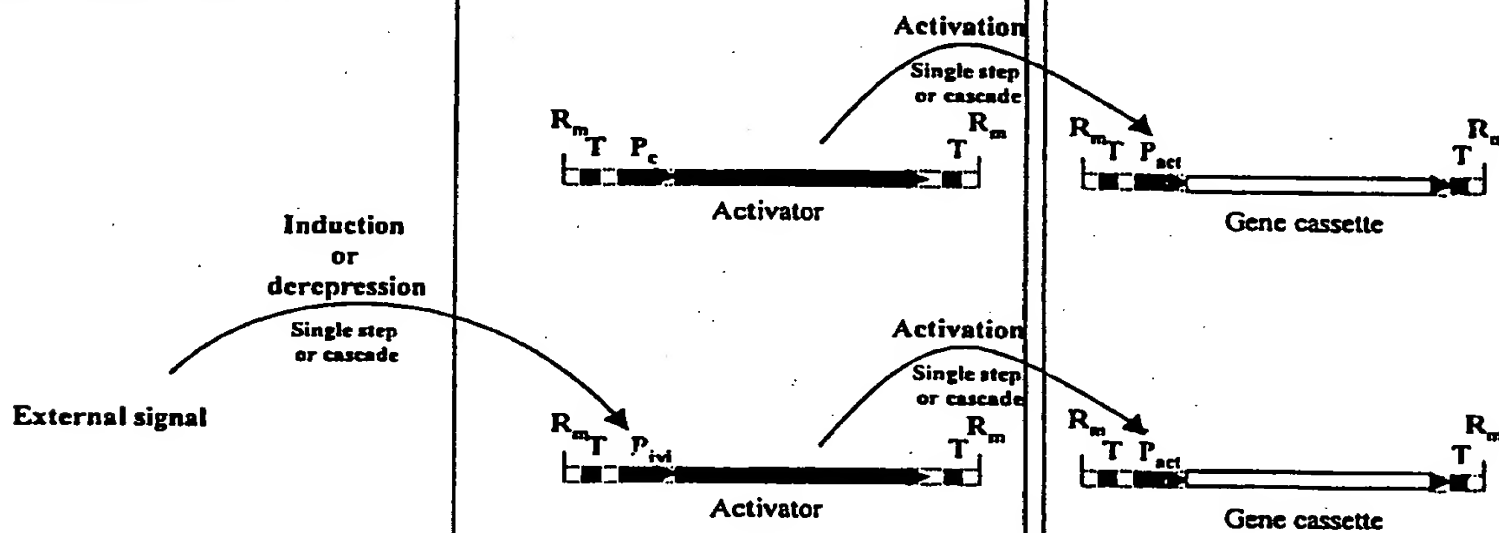
- P = Promoter consisting of either a
- promoter acting constitutively in *Salmonella*
 - a *Salmonella in vivo* inducible promoter or
 - an other promoter

P_c = Constitutive promoter

P_{in} = In vivo inducible promoter

P_{act} = Activatable promoter

One Phase System



Two Phase System

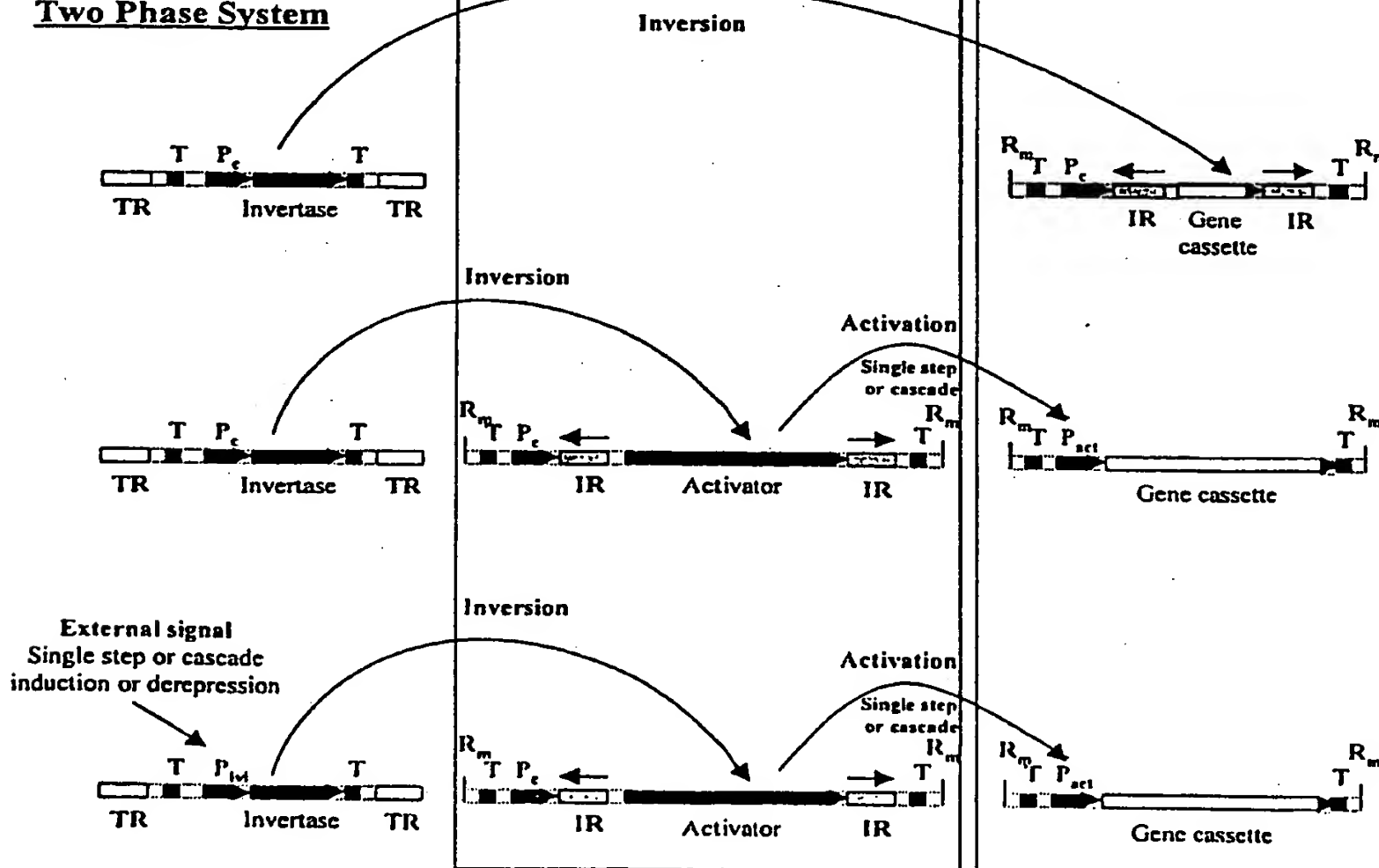


Figure 21

Fig. 21A

CTGCAGTTGTCCGGTTATTGCTCGTCAAGCGAACAGATGCAAAAGGTGAGAGCGACTCTCGAATCATGGGGGGTTCATGTA
TCGGGATGGTGTAACTCTGTGATGACTTATTGGTACGAGAAGTGCAGGATGTTTTGATAAAAATGGGTTACCCGCGATGCTG
AAGTATCCAGCGAAGGGCCGGGGAGCGTGTTAATTCATGATGATATACAAATGGATCAGCAATGGCGCAAGGTTCAACCA
TTACTTGCAGATATTCCCGGGTTATTGCACTGGCAGATTAGTCACTCTCATCAGTCTCAGGGGGATGATATTATTTCTGC
GATAATAGAGAACGGTTTAGTGGGGCTTGTCAATGTTAGCCCAATGCGGCGCTCTTTTGTATCAGTGGTGTACTGGATG
AATCTCATCAACGCATTTTGAAGAAACGTTAGCAGCATTAAAGAAAAGGATCCCGCTCTTTCTTTAATTTATCAGGAT
ATTGCGCCTTCCCATGATGAAAGCAAGTATCTGCCTGCGCCAGTGGCTGGCTTTGTACAGAGTCGCCATGGTAATTACTT
ATTACTGACGAATAAAGAGCGTTTACGTGTAGGGGCATTGTTACCCAATGGGGGAGAAATTGTCCATCTGAGTGCCGATG
TGGTAACGATTAAACATTATGATACTTTGATTAATCTATCCATTAGATTTTAAGTGAGTGGAATGACAACCTTTGACCCG
GTTAGAAGATTTGCTGCTTCATTGCGGTGAAGAGGCCAAAGGCATAATTTTACAATTAAGGGCTGCCCGGAAACAGTTAG
AAGAGAACAACGGCAAGTTACAGGATCCGCAGCAATATCAGCAAAACACCTTATTGCTTGAAGCGATCGAGCAGGCCGAA
AATATCATCAACATTATTTATTATCGTTACCATAACAGCGCACTTGTAGTGAGTGAGCAAGAGTAAAGTAAAAATATCTT
AGAGCCTATCCCACCAGGCGTTAATTGGCGCAGCCAGTTTGGACACGGATAGCGCGCAAAAACCGCAGCGTACACGTAGT
ACGTGAGGTTTGACTCGCTACGCTCGCCCTTCGGGCGCGCTAGCGGCGTTCAAAACGCTAACGCGTTTGGCGAGCAC
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GGAGGGGAATGATGATAAAGAAAAAGGCTGCGTTTAGTGAATATCGTGATTTAGAGCAAAGTTACATGCAGCTAAATCAC
TGTCTTAAAAAATTTACCAAATCCGGGCTAAGGTGAGTCAACAGCTTGCTGAAAGGGCAGAGAGCCCCAAAAATAGCAG
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TGAGGATGTAATTAATAACATGCGTGATAATGGTATTCTCATCGATGGTATGACCATTGATGATTATATGGCTAAATATG
GCGATCATGGGAAGCTGGATAAAGGTGGCCTACAGGCGATCAAAGCGGCTTTGGATAATGACGCCAACCGGAATACCGAT
CTTATGAGTCAGGGGCAGATAACAATTCAAAAAATGTCTCAGGAGCTTAACGCTGTCTTACCCAAGTACAGGGCTTAT
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TGACACGATGCGGTTTTTCCGGCGTGCGGCTCGCTGCGTATGTTGTTGGATGACGATGTTACACAGCCGCTTAATACTC
TGTATCGCTATGCCACGCAGCTTATGGAGGTAAAGAATTGCGCGGCGCAGCGCGACTTTTTCAATTGCTGACGATATAT
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ACGTCTGTTATGCAATCAAAGCGTTAAAGGCCGTGGTGCGTATTTGCGGCGAGGTGAGTGAACATCAAATTTCTCCGACAG
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GGAGTAACCGCCTTAACACATCATCACTTAAGCAATGTCAGTTGCGTTTTCTCGGGTTGCTGGGAAAGCGCCAGCATCG
TGTGAATTTCTACTTTTGGCGATGGCAACGCCGCGTGTCTGCTATCCGGGAAATTAGTCTTCAGGAGGCAAGCAATGCGT
TGAAGCAACTGCTTGATGCCGTACCCGGAAATCATAAGCGTCCATCATTGCCTGACTTTTTGACAGCAATCCCGCGGTT
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GTAAGATTCAATTTGGTTGTGAAGCCGTGCGCTGGCACTGGATGTTTTCCAGATTGGCCGTGCTTTTATGGCGACGAGA
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GCGAGTAACGTAGCACTGGTATTACCAGCGCCTTCTTGTTAACACCTTCTTCCACTCCATCTCCCTCCGGGGAGGGAAAT
GGGTACTGAATCAATGCTTCTGTTATTTGATGATATCTGGATGAAGCTAATGGAGCTTGCCAAAAAGCTGCGCGATATCA
TGCGCAGCTATAACGTAGAAAAACAACGGCTGGCCTGGGAACTGCAAGTCAATGTTTTACAGACGCAATGAAAACAATT
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CGCAACGTCAAAGTGATCAAGATAAAGCGATTGCCGACCTGCAACAAAATGGGGCCCAATCTTATAATAAATCCCTGACG
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TCAGATGGAGGGCGTGATTAATGCAAAAGTGACCATTGCGCTACCGACTTATGATGAGGGAAGTAACGCTTCTCCGAGCT
CAGTTGCCGTATTTATAAAATATTCACCTCAGGTCAATATGGAGGCCTTTCCGGTAAAAATTAAAGATTTAATAGAGATG
TCAATCCCTGGGTTGCAATACAGTAAGATTAGTATCTTGATGCAGCCTGCTGAATTC

Fig. 21B

AGCATTGACATAAAAACTTACAATTTGAAAAATTATTTATTAAATAAACTGTTACGATGTTTTTACATCGCCATCTTATT
AAAAAGTAATTGTAGTCATCGACTGGGTTATATATGAAGAAATTTATCTTCCTAATGATAACACCATCGATTAATCTTCT
GATGAAACTATATGTACTGCGATAGTGATCAAGTGCCAAAGATTTTGCAACAGGCAACTGGAGGGAAGCATTATGAATTT
GCTCAATCTCAAGAATACGCTGCAAACATCTTTAGTAATCAGGCTAACTTTTTTTATTTTATTAACAACAATAATTATTT
GGCTGCTATCTGTGCTTACCGCAGCTTATATATCAATGGTTTCAAGAACGGCAGCATATAATAGAGGATTTATCCGTTCTA
TCCGAGATGAATATTGTACTAAGCAATCAACGGTTTGAAGAAGCTGAACGTGACGCTAAAAATTTAATGTATCAATGCTC
ATTAGCGACTGAGATTCATCATAACGATATTTTCCCTGAGGTGAGCCGGCATCTATCTGTGCGTCCTTCAAATTGCACGC
CGACGCTAAACGGAGAGAAGCACCGTCTCTTTCTGCAGTCCTCTGATATCGATGAAAATAGCTTTCGTGCGGATAGTTTT
ATTCTTAATCATAAAAAATGAGATTTTCGTTATTATCTACTGATAACCCTTCAGATTATTCAACTCTACAGCCTTTAACGCG
AAAAAGCTTTCTTTTATACCCAACCCATGCCGGGTTTTACTGGAGTGAACCAGAATACATAAACGGCAAAGGATGGCAGC
CTTCCGTTGCGGTTGCCGATCAGCAAGGCGTATTTTTTGAGGTGACGGTTAAACTTCCCGATCTCATTACTAAGAGCCAC
CTGCCATTAGATGATAGTATTCGAGTATGGCTGGATCAAAACAACCACTTATTGCCGTTTTTCATACATCCCGCAAAAAAT
ACGTACACAGTTAGAAAATGTAACGCTGCATGATGGATGGCAGCAAATTTCCCGGATTTCTGATATTACGCACAACCTTGC
ATGGCCCCGGATGGAGTCTGGTTACGCTGTACCCATACGGTAATCTACATAATCGCATCTTAAAAATTATCCTTCAACAA
ATCCCCTTTACATTAACAGCATTGGTGTGATGACGTCGGCTTTTTTGCTGGTTACTACATCGCTCACTGGCCAAACCGTT
ATGGCGTTTTGTGCGATGTCATTAATAAAACCGCAACTGCACCGCTGAGCACACGTTTTACCAGCACAAACGACTGGATGAAT
TAGATAGTATTGCCGGTGCTTTTAAACCAACTGCTTGATACTCTACAAGTCCAATACGACAATCTGGAAAACAAAGTCGCA
GAGCGCACCCAGGCGCTAAATGAAGCAAAAAACGCGCTGAGCGAGCTAACAAACGTAAAAGCATTCTTACGGTAAT
AAGTCATGAGTTACGTACTCCGATGAATGGCGTACTCGGTGCAATTGAATTATTACAAACCACCCCTTTAAACATAGAGC
AACAAAGGATTAGCTGATACCGCCAGAAATTGTACACTGTCTTTGTTAGCTATTATTAATAATCTGCTGGATTTTTTCACGC
ATCGAGTCTGGTCATTTTACATTACATATGGAAGAAACAGCGTTACTGCCGTTACTGGACCAGGCAATGCAAACCATCCA
GGGGCCAGCGCAAAGCAAAAACTGTCAATTACGTACTTTTGTGCGGTCAACATGTCCCTCTCTATTTTTCATACCGACAGTA
TCCGTTTACGGCAAATTTTGGTTAATTTACTCGGGAACGCGGTAAAATTTACCGAAACCGGAGGGATACGTCTGACGGTC
AAGCGTCATGAGGAACAATTAATATTTCTGGTTAGCGATAGCGGTAAAGGGATTGAAATACAGCAGCAGTCTCAAATCTT
TACTGCTTTTTTATCAAGCAGACACAAATTCGCAAGGTACAGGAATTGGACTGACTATTGCGTCAAGCCTGGCTAAAATGA
TGGGCGGTAAATCTGACACTAAAAAGTGTCCCCGGGGTTGGAACCTGTGTCTCGCTAGTATTACCCTTACAAGAATACCAG
CCGCCTCAACCAATTAAGGGACGCTGTGACGCGCGTTCTGCCTGCATCGGCAACTGGCTTGCTGGGGAATACGCGGTGA
ACCACCCACCAGCAAAATGCGCTTCTCAACGCAGAGCTTTTGTATTTCTCCGAAAACCTCTACGACCTGGCGCAACAGT
TAATATTGTGTACACCAAATATGCCAGTAATAAATAATTTGTTACCACCCTGGCAGTTGCAGATTCTTTTGGTTGATGAT
GCCGATATTAATCGGGATATCATCGGCAAAATGCTTGTGACCTGGGCAACACGTCATATTGCCGCCAGTAGTAACGA
GGCTCTGACTTTATCACAACAGCAGCGATTTCGATTTAGTACTGATTGACATTAGAATGCCAGAAATAGATGGTATTGAAT
GTGTACGATTATGGCATGATGAGCCGAATAATTTAGATCCTGACTGCATGTTTGTGGCACTATCCGCTAGCGTAGCGACA
GAAGATATTCATCGTTGTAAAAAAATGGGATTCATCATTACATTAACAAACAGTGACATTGGCTACCTTAGCTCGCTA
CATCAGTATTGCCGCAGAATACCAACTTTTACGAAATATAGAGCTACAGGAGCAGGATCCGAGTCGCTGCTCAGCGCTAC
TGGCGACAGATGATATGGTCATTAATAGCAAGATTTTCCAATCACTGGACCTCTTGCTGGCTGATATTGAAAATGCCGTA
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AGAGCATGTTAAAAATGGTCTTGAGGTTTATAATGCCTGTTGTGCATACGAGCCTGACATACTTATCCTTGATCTTAGTC
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TCTGTTAGCGGCATTGCAAACAGTAGCAGTAAACAAGCGTTACATTGACCCAACGTTGAATCGGGAAGCTATCCTGGCTG
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ACAGGTTTATAAAGTGACAGAGTTACTTAACTGTGCCCGAAGAATGAGGTTAATAGAGTATTAACCAGGGGGCGTCCGATG
GTATTAAGCATTGGTCATATTTTGTATGAGCCTTACGCCACGCAGTATTGCTCATCATCGACAAAAATCCATACGGATGCCC
TGGTATGCCGCACCATTATCACTACCTTAGTCTTCATTTGATCATGATATAGTAGAATCCCCTTATTTAACGGGCTTTA
CCATGTCGTATTCTATCGGCGAATTTGCCAGACTATGCGGTATCAATGCCGCCACGCTAAGGGCATGGCAGCGACGCTAT
G

Figure 22

Fig. 22A

sseA

ATGATGATAAAGAAAAAGGCTGCGTTTAGTGAATATCGTGATTTAGAGCAAAGTTACATGCAGCTAAATCACTGTCTTAA
AAAATTTACCAAATCCGGGCTAAGGTGAGTCAACAGCTTGCTGAAAGGGCAGAGAGCCCCAAAAATAGCAGAGAGACAG
AGAGTATTCTTCATAACCTATTTCCACAAGGCGTTGCCGGGGTTAACCAGGAGGCCGAGAAGGATTTAAAGAAAAATAGTA
AGTTTGTTTAAACAACCTTGAAGTACGACTGAAACAACCTTAATGCTCAAGCCCCGGTGGAGATACCGTCAGGAAAAACAAA
AAGGTAA

Fig. 22B

sseB

ATGTCTTCAGGAAACATCTTATGGGGAAGTCAAAACCCTATTGTGTTTAAAAATAGCTTCGGCGTCAGCAACGCTGATAC
CGGGAGCCAGGATGACTTATCCAGCAAAATCCGTTTGCCGAAGGGTATGGTGTGTTTGCTTATTCTCCTTATGGTTATTC
AGGCTATCGCAAATAATAAATTTATTGAAGTCCAGAAGAACGCTGAACGTGCCAGAAATACCCAGGAAAAGTCAAATGAG
ATGGATGAGGTGATTGCTAAAGCAGCCAAAGGGGATGCTAAAACCAAAGAGGAGGTGCCTGAGGATGTAATTAAATACAT
GCGTGATAATGGTATTCTCATCGATGGTATGACCATTGATGATTATATGGCTAAATATGGCGATCATGGGAAGCTGGATA
AAGGTGGCCTACAGGCGATCAAAGCGGCTTTGGATAATGACGCCAACCGGAATACCGATCTTATGAGTCAGGGGCAGATA
ACAATTCAAAAAATGTCTCAGGAGCTTAACGCTGTCCTTACCCAACCTGACAGGGCTTATCAGTAAGTGGGGGGAATTTTC
CAGTATGATAGCGCAGAAAACGTACTCATGA

Fig. 22C

sseC

ATGAATCGAATTCACAGTAATAGCGACAGCGCCGAGGAGTAACCGCCTTAACACATCATCACTTAAGCAATGTCAGTTG
CGTTTCCTCGGGTTCGCTGGGAAAGCGCCAGCATCGTGTGAATCTACTTTTGGCGATGGCAACGCCGCGTGTCTGCTAT
CCGGGAAAATTAGTCTTCAGGAGGCAAGCAATGCGTTGAAGCAACTGCTTGATGCCGTACCCGGAAATCATAAGCGTCCA
TCATTGCTGACTTTTTGCGAGACCAATCCCGCGGTTTTATCAATGATGATGACGTCATTAATACTCAACGTCTTTGGTAA
TAACGCTCAATCGTTATGCCAACAGCTTGAGCGGGCAACTGAGGTGCAAAATGCATTACGTAATAAGCAGGTAAAGGAGT
ATCAGGAGCAGATCCAGAAAGCGATAGAGCAGGAGGATAAAGCGCGTAAAGCGGGTATTTTTGGCGCTATTTTTGACTGG
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GTTTTCCAGATTGGCCGTGCTTTTTATGGCGACGAGAGGTTTATCTGGCGCAGCTGCAAAAGTGCTTGACTCCGGTTTTGG
CGAGGAAGTGGTTGAGCGTATGGTAGGTGCAGGGGAAGCAGAAATAGAGGAGTTGGCTGAAAAGTTTGGCGAAGAAGTGA
GCGAAAGTTTTTCCAAACAATTTGAGCCGCTTGAACGTGAAATGGCTATGGCGAATGAGATGGCAGAGGAGGCTGCCGAG
TTTTCTCGTAACGTAGAAAATAATATGACGCGAAGCGCGGGAAAAAGCTTTACGAAAGAGGGGGTGAAAGCCATGGCAAA
AGAAGCGGCAGAAAGAGCCCTGGAAAAATGTGTGCAAGAAGGTGGAAAGTTCTGTAAAAAAATTCGGTAATAAAGTTC
TCTTCAATATGTTCAAAAAAATCCTGTATGCCTTACTGAGGGATTGTTCAATTTAAAGGCTTACAGGCTATCAGATGTGCA
ACCGAGGGCGCCAGTCAGATGAATACTGGCATGGTTAACACAGAAAAAGCGAAGATCGAAAAGAAAATAGAGCAATTAAT
AACTCAGCAACGGTTTCTGGATTTTATAATGCAACAAACAGAAAACAGAAAAAGATAGAACAAAAACGCTTAGAGGAGC
TTTATAAGGGGACGGGTGCCGCGCTTAGAGATGTATTAGATACCATTGATCACTATAGTAGCGTTCAGGCGAGAATAGCT
GGCTATCGCGCTTAA

Fig. 22D

sseD

ATGGGTACTGAATCAATGCTTCTGTTATTTGATGATATCTGGATGAAGCTAATGGAGCTTGCCAAAAAGCTGCGCGATAT
CATGCGCAGCTATAACGTAGAAAAACAACGGCTGGCCTGGGAACTGCAAGTCAATGTTTTACAGACGCAAATGAAAACAA
TTGATGAAGCGTTTAGAGCATCAATGATTACTGCGGGTGGCGCAATGTTGTGCGGGTGTACTGACGATAGGATTAGGGGCC
GTAGGCGGGGAAACCGGTCTTATAGCGGGTCAAGCCGTAGGCCACACAGCTGGGGGCGTCATGGGCCTGGGGGCTGGTGT
AGCGCAACGTCAAAGTGATCAAGATAAAGCGATTGCCGACCTGCAACAAAATGGGGCCCAATCTTATAATAAATCCCTGA
CGGAAATTATGGAGAAAGCAACTGAAATTATGCAGCAAATCATCGGCGTGGGGTCGTCAGTGGTCACGGTTCTTGCTGAA
ATACTCCGGGCATTAACGAGGTAA

Fig. 22E

sseE

ATGGTGCAAGAAATAGAGCAATGGTTACGTCCGGCATCAGGTGTTTACTGAGCCTGCATATTTAGGGGAGACCGCCATATT
 ACTTGGGCAGCAGTTTATATTATCGCCTTACCTGGTGATCTATCGTATTGAGGCAAAAGAAATGATTATTTGTGAGTTCA
 GGCGCCTGACGCCCCGGGCAACCTCGACCACAGCAATTGTTTCACTTACTGGGACTTTTACGCGGGATATTTGTGCATCAC
 CCGCAGTTAACATGTTTAAAGATGTTGATAATCACCGACGTTCTGGATGAAAAAAAAGCCATGCTACGCAGGAAATTATT
 GCGCATCCTGACAGTAATGGGAGCGACCTTTACACAGCTTGATGGCGATAACTGGACAGTTTTATCCGCCGAGCATCTTA
 TCCAGCGACGTTTTTAA

Fig. 22F

sseF

ATGAAAATTCATATTCCGTCAGCGGCAAGTAATATAGTCGATGGTAATAGTCCTCCTTCCGATATACAAGCGAAGGAGGT
 ATCGTTTTCTCCCCCTGAAATTCCAGCGCCTGGCACCCCCGAGCCCCCTGTGCTGCTTACGCCTGAACAAATAAGGCAGC
 AGAGGGATTATGCGATACATTTTATGCAATACACTATTCGTGCGCTGGGTGCGACAGTCGTGTTGGGTATCGGTTGCT
 GCAGCGGTAATTTCTGGCGGGGAGGATTACCCATTGCTATTCTTGCGGGGGCGGCGCTCGTGATTGCTATTGGGGATGC
 TTGCTGTGCGTATCATAATTATCAATCGATATGTCAGCAAAAGGAGCCATTACAAACCGCCAGTGATAGCGTTGCTCTTG
 TGGTCAGTGCGCTGGCCTTAAATGTGGGGCAAGTCTTAAGTGCCTAACACCCTTGCTAATTGTCTTTCTTTATTAATA
 CGTTCAGGAATCGCTATTTCTATGTTGGTTTTACCCCTACAGTTTCCACTGCCCCGCGGCTGAAAATATTGCGGCCTCTTT
 GGACATGGGGAGTGTAATTACCTCCGTTAGCCTGACGGCGATAGGTGCGGTACTGGATTATTGCCTTGCCCCGCCCTCTG
 GCGACGATCAGGAAAATTCTGTTGATGAACTTCATGCCGATCCCAGTGTGTTATTGGCGGAACAAATGGCAGCGCTCTGT
 CAATCTGCTACTACACCTGCACCTGCATTAATGGACAGTTCTGATCATACATCTCGGGGAGAACCATGA

Fig. 22G

sseG

ATGAAACCTGTTAGCCCAAATGCTCAGGTAGGAGGGCAACGTCCTGTTAACGCGCCTGAGGAATCACCTCCATGTCCTTC
 ATTGCCACATCCGGAAACCAATATGGAGAGTGGTAGAATAGGACCTCAACAAGGAAAAGAGCGGGTATTGGCCGGACTTG
 CGAAACGAGTGATAGAGTGTTCCTCAAAGAAATTTTAGTTGGCAAACGGTTATTTTGGGCGGACAGATTTTATGCTGT
 TCCGCTGGAATAGCATTAAAGTGCTAAGTGGTGGAGGCGCGCGCTCGTAGCCCTGGCAGGGATTGGCCTTGCTATTGC
 CATCGCGGATGTCGCCTGTCTTATCTACCATCATAAACATCATTTGCCTATGGCTCACGACAGTATAGGCAATGCCGTTT
 TTTATATTGCTAATTGTTTCGCCAATCAACGCAAAAGTATGGCGATTGCTAAAGCCGTCTCCCTGGGCGGTAGATTAGCC
 TTAACCGCGACGGTAATGACTCATTACACTGGAGTGGTAGTTTGGGACTACAGCCTCATTTATTAGAGCGTCTTAATGA
 TATTACCTATGGACTAATGAGTTTTACTCGCTTCGGTATGGATGGGATGGCAATGACCGGTATGCAGGTCAGCAGCCCAT
 TATATCGTTTTGCTGGCTCAGGTAACGCCAGAACAACGTGCGCCGGAGTAA

Fig. 22H

ssCA

ATGAAAAAAGACCCGACCCTACAACAGGCACATGACACGATGCGGTTTTTCCGGCGTGCGGGCTCGCTGCGTATGTTGTT
 GGATGACGATGTTACACAGCCGCTTAATACTCTGTATCGCTATGCCACGCAGCTTATGGAGGTAAAAGAATTCGCCGGCG
 CAGCGCGACTTTTTCAATTGCTGACGATATATGATGCCTGGTCATTTGACTACTGGTTTTCGGTTAGGGGAATGCTGCCAG
 GCTCAAAAACATTGGGGGGAAGCGATATACGCTTATGGACGCGCGGCACAAATTAAGATTGATGCGCCGCGAGGCGCCATG
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 GCGAGGTCAGTGAACATCAAATCTCCGACAGCGTGAGAAAAGATGTTACAGCAACTTTCTGACAGGAGCTAA

Fig. 22I

ssCB

ATGATGATGAAAGAAGATCAGAAAAATAAAATACCCGAAGACATTCTGAAACAGCTATTATCCGTTGATCCGGAAACCGT
 TTATGCCAGTGGTTACGCCTCATGGCAGGAGGGGGATTATTCGCGCGCCGTAATCGATTTTAGTTGGCTGGTGATGGCCC
 AGCCATGGAGTTGGCGTGCCCATATTGCATTGGCTGGCACCTGGATGATGCTTAAAGAATACACGACGGCCATTAATTC
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 ACCCGGGTTGGCGAGAGAGGCTTTTCAAACCGCAATCAAGATGAGTTATGCGGATGCCTCATGGAGTGAGATTCCGCCAGA
 ATGCGCAATAATGGTTGATACTCTTATTGCTTAA

Fig. 22J

ssaD

ATGGCATATCTCATGGTTAATCCAAAGAGTTCCTGGAAAATACGTTTTTTTAGGTCACGTTTTTACAAGGCCGGGAAGTATG
GCTGAATGAAGGTAACCTGTCACTGGGGGAGAAGGGATGCGATATTTGTATTCCGCTGGCTATAAATGAAAAAATTATTC
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CCAATGGGGGAGAAATTGTCCATCTGAGTGCCGATGTGGTAACGATTAAACATTATGATACTTTGATTAACCTATCCATTA
GATTTTAAGTGA

Fig. 22K

ssaE

ATGACAACCTTTGACCCGGTTAGAAGATTTGCTGCTTCATTCGCGTGAAGAGGCCAAAGGCATAATTTTACAATTAAGGGC
TGCCCGGAAACAGTTAGAAGAGAACAACGGCAAGTTACAGGATCCGCAGCAATATCAGCAAAACACCTTATTGCTTGAAG
CGATCGAGCAGGCCGAAAATATCATCAACATTATTTATTATCGTTACCATAACAGCGCACTTGTAGTGAGTGAGCAAGAG
TAA

Fig. 22L

ssaG

ATGGATATTGCACAATTAGTGGATATGCTCTCCACATGGCGCACCAGGCAGGCCAGGCCATTAATGACAAAATGAATGG
TAATGATTTGCTCAACCCAGAATCGATGATTAAAGCGCAATTTGCCTTACAGCAGTATTCTACATTTATTAATTACGAAA
GTTCACTGATCAAAATGATCAAGGATATGCTTAGTGGAATCATTGCTAAAATCTGA

Fig. 22M

ssaH

ATGTTTGCGGGCGTTAACCATAGCCTGATTTCCCAGGTACATGCGATGTTACCAGCGCTAACGGTTATTGTTCCGGATAA
AAAATTACAGTTGGTATGTCTGGCATTATTGTTGGCGGGTTTAAATGAGCCGCTAAAAGCCGCGAAAATTTTATCGGATA
TAGATTTGCCAGAGGCTATGGCGCTGCGTCTGTTATTTCTGCACCAAATGAGGGGTTTGAAAATTGA

Fig. 22N

ssaI

ATGAGCGTAGTGCTGTAAAGCACTCAATCTTATGTAAAGTCCTCTGCAGAACCGAGCCAGGAGCAAATTAATTTTTTTGA
ACAATTGCTGAAAGATGAAGCATCCACCAGTAACGCCAGTGCTTTATTACCGCAGGTTATGTTGACCAGACAAATGGATT
ATATGCAGTTAACGGTAGGCGTCGATTATCTTGCCAGAATATCAGGCGCAGCATCGCAAGCGCTTAATAAGCTGGATAAC
ATGGCATGA

Fig. 22O

ssaJ

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GCCAGAAGATGAAGCGAATCAAATGCTGGCATTACTTATGCAGCATCATATTGATGCGGAAAAAAACAGGAAGAGGATG
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TGAATTCAGAATGGTAGCTGACGTACCCGCGAGACAAACATTCTGGATTATGGACGTTATCAACGCCAATAAAGGGAAGG
TGGTGAAGTGGTTGATGAAATACCTTATCCGTTGATGTTATCGTTGACAGGACTGTTATTAGGAGTGGGCATCCTGATC
GGCTATTTTTGCTGAGACGCCGTTTTTGA

Fig. 22P

ssrA

ATGAATTTGCTCAATCTCAAGAATACGCTGCAAACATCTTTAGTAATCAGGCTAACTTTTTTATTTTATTATTAACAACAAT
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CCGTTCTATCCGAGATGAATATTGTACTAAGCAATCAACGGTTTGAAGAAGCTGAACGTGACGCTAAAAATTTAATGTAT
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CCAGAAAAATACGTATGATCTTCAAAAACTACACCATTACTTAA

Fig. 22Q

ssrB

ATGAAAGAATATAAGATCTTATTAGTAGACGATCATGAAATCATCATTAAACGGCATTATGAATGCCTTATTACCCTGGCC
TCATTTTAAAATTGTAGAGCATGTTAAAAATGGTCTTGAGGTTTATAATGCCTGTTGTGCATACGAGCCTGACATACTTA
TCCTTGATCTTAGTCTACCTGGCATCAATGGCCTGGATATCATTCTCAATTACATCAGCGTTGGCCAGCAATGAATATT
CTGGTTTACACAGCATAACCAACAAGAGTATATGACCATTAAACTTTAGCCGCAGGTGCTAATGGCTATGTTTTAAAAAG
CAGTAGTCAGCAAGTTCTGTTAGCGGCATTGCAAACAGTAGCAGTAAACAAGCGTTACATTGACCCAACGTTGAATCGGG
AAGCTATCCTGGCTGAATTAAACGCTGACACGACCAATCATCAACTGCTTACTTTGCGCGAGCGTCAGGTTCTTAAACTT
ATTGACGAGGGGTATACCAATCATGGGATCAGCGAAAAGCTACATATCAGTATAAAAACCGTCGAAACACACCGGATGAA
TATGATGAGAAAGCTACAGGTTTATAAAGTGACAGAGTTACTTAACTGTGCCCCGAAGAATGAGGTTAATAGAGTATTAA

Figure 23

Fig. 23A

SseA

MMIKKKAAFSEYRDLEQSYMQLNHCLKKFHQIRAKVSQQLAERAESPKNRETESI LHNLFPOGVAGVNQEAEDLKKIV
SLFKQLEVRLKQLNAQAPVEIPSGKTKR

Fig. 23B

SseB

MSSGNILWGSQNPIVFKNSFGVSNADTGSQDDLSQQNPFAEGYGVLLILLMVIQAIANNKFIEVQKNAERARNTQEKSNE
MDEVIAKAAKGDAKTKEEVPEDVIKYM RDNGILIDGMTIDDYMAKYGDHGKLDKGGLQAIKAALDNDANRNTDLMSQGQI
TIQKMSQELNAVLTLTGLISKWGEISSMIAOKTYS

Fig. 23C

SseC

MNRIHSNSDSAAGVTALTHHLSNVSCVSSGSLGKRQHRVNSTFGDGNAACLLSGKISLQEASNALKQLLDVPGNHKRP
SLPDFLQTNPAVLMMMTSLILNVFGNNAQSLCQQLERATEVQNALRNKQVKEYQEQIQKAIEQEDKARKAGIFGAI FDW
ITGIFETVIGALKVVEGFLSGNPAEMASGVAYMAAGCAGMVKAGAETAMMCGADHDTQAIIDVTSKIQFGCEAVALALD
VFQIGRAFMATRGLSGAAAKVLD SGFGEEVVERMVGAGEAEIEELAEKFGEVSESF SKQFEPLEREMAMANEMAE EAAE
FSRNVENNMTRSAGKSFTKEGVKAMAKEAAKEALEKCVQEGGKFLKKFRNKVLFNMFKKILYALLRDCSFKGLQAIRCA
TEGASQMNTGMVNTTEKAKIEKKIEQLITQQRFLDFIMQQTENQKKIEQKRLEELYKGTGAALRDVLD TIDHYSSVQARIA
GYRA

Fig. 23D

SseD

MEASNVALVLPAPSLLTSPSPSGEGMGTESMLLLFDDIWMKLMELAKKL RDIMRSYNVEKQRLAWELQVNVLOTQMK
TIDEAFRASMITAGGAMLSGVLTIGLGAVGGETGLIAGQAVGHTAGGVMGLGAGVAQRQSDQDKAIADLQONGAQSYNKS
LTEIMEKATEIMQQIIGVGSSSLVTVLAEILRALTR

Fig. 23E

SseE

MVQEI EQWLRRHQVFTEPAYLGETAILLGQQFILSPYLVIYRIEAKEMIICEFRRLTPGQPRPQQLFHLLGLLRGIFVHH
PQLTCLKMLIITDVLDEKKAMLRRLRLTVMGATFTQLDGDNWTVLSAEHLIQRRF

Fig. 23F

SseF

MKIHIPSAASNIVDGNSPPSDIQAKEVSFPPEIPAPGTPAAPVLLTPEQIRQQRDYAIHFMQYTTIRALGATVVFGLSVA
AAVISGGAGLPAILAGAAALVIAIGDACCAYHNYQSICQOKEPLOTASDSVALVVSALALKCGASLNCANTLANCLSLLI
RSGIAISMLVLPLOFPLPAAENIAASLDMGSVITSVSLTAIGAVLDYCLARPSGDDQENSVDLHADPSVLLAEQMAALC
QSATTPAPALMDSSDHTSRGEP

Fig. 23G

SseG

MKPVSPNAQVGGQRPVNAPEESPPCPSLPHPETNMESGRIGPOQGKERVLAGLAKRVIECFPKEIFSWQTVILGGQILCC
SAGIALTVLSGGGAPLVALAGIGLAIAIADVACLIYHHKHLPMAHDSIGNAVFYIANCFANQRKSMAIAKAVSLGGRLA
LTATVMTHSYWSGSLGLQPHLLERLNDITYGLMSFTRFGMDGMAMTGMQVSSPLYRLLAQVTPEQRAPE

Fig. 23H

SscA

MKKDPTLQQAHDTMRFFRRGGSRLMLLDDDDVTQPLNTLYRYATQLM EVKEFAGAARLFQLLTIYDAWSFDYWFR LG ECCQ
AQKHWGEAIYAYGRAAQIKIDAPQAPWAAAECYLACDNVCYAIKALKAVVRICGEVSEHQILRQRAEKMLQQLSDRS

Fig. 23I

SscB

MMMKEDQKNKIPEDILKQLLSVDPETVYASGYASWQEGDYSRAVIDFSWLVMAPWSWRAHIALAGTWMMLKEYTTAINF
YGHALMLDASHPEPVYQTGVCLKMMGEPGLAREAFQTAIKMSYADASWSEIRQNAQIMVDTLIA

Fig. 23J

SsaD

MAYLMVNP KSSWKIRFLGHV LQGREVWLN EGNLSLGEKGC DICIPLAINEKIILREQADSLFVDAGKARVRVNGRRFNP
 KPLPSSGV LQVAGVAIAFGKQDCELADYQIPVSRSGYWLAGVFLIFIGGMGVLLSISGQPETVNDLPLRVKFLLDKSNI
 HYVRAQWKEDGSLQLSGYCSSEQMOKVRATLESWGVMYRDGVICDDLLVREVQDVLIKMGYPHAEVSSEGPSVLIHDD
 IQMDQQWRKVQPLLADIPGLLHWQISHSHQSQGDDIISAI IENGLVGLVNVSPMRRSFVISGVLDESHQRILQETLAALK
 KKDPALSLIYQDIAPSHDESKYLPAPVAGFVQSRHGNYLLLTN KERLRVGALLPNGGEIVHLSADVVTIKHYDTLINYPL
 DFK

Fig. 23K

SsaE

MTTLTRLEDLLLHSREEAKGIILQLRAARKQLEENNGKLQDPQQYQQNTLLLEAIEQAENIINI IYYRYHNSALVVSEQE

Fig. 23L

SsaG

MDIAQLVDMLSHMAHQAGQAINDKMNGNDLLNPESMIKAQFALQQYSTFINYESSLIKMIKDMLSGIIAKI

Fig. 23M

SsaH

MFAGVNHSLISQVHAMPALTVIVPDKKLQLVCLALLLAGLNEPLKAAKILSDIDLPEAMALRLLFPAPNEGFEN

Fig. 23N

SsaI

MSVVPVSTQSYVKSSAEPSEQEINFFEQLLKDEASTSNASALLPQVMLTRQMDYMQLTVGVDYLARISGAASQALNKLDN
 MA

Fig. 23O

SsaJ

MKVHRIVFLTVLTFFLTACDVDLYRSLPEDEANQMLALLMQHHIDAEEKQEEDGVTLRVEQSQFINAVELLRLNGYPHRQ
 FTTADKMFANQLVVSPQEEQQKINFLKEORIEGMLSQMEGVINAKVTIALPTYDEGSNASPSSVAVFIKYSPOVNMEAF
 RVKIKDLIEMSIPGLQYSKISILMQPAEFRMVADVPARQTFWIMDVINANKGKVVKWLMKYPYPLMLS LTGLLLGVGILI
 GYFCLRRRF

Fig. 23P

SsrA

MNLLNLKNTLQTSLVIRLTFLFLLTTIIIWLLSVLTAAYISMVQKROHIIEDLSVLSEMNIIVLSNQRFEAAERDAKNLMY
 QCSLATEIHNDIFPEVSRHLSVGPSNCTPTLNGEKHRLFLQSSDIDENSFRDSSFILNHKNEISLLSTDNP SDYSTLQP
 LTRKSFPLYPTHAGFYWSEPEYINGKGWHASVAVADQQGVFFEVTVKLPDLITKSHLPLDDSI RVWLDQNNHLLPFSYIP
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 SNEALTLSQQQRFDLVLIDIRMPEIDGIECVRLWHDEPNNDLPDCMFVALSASVATEDIHRCKKNGIHHYITKPVTLATL
 ARYISIAAEYQLLRNIELQEODPSRCSALLATDDMVINSKIFQSLDLLLADIENAVSAGEKIDQLIHTLKGCLGQIGQTE
 LVCYVIDIENRVKMGKIIALEELTDLRQKIRMIFKNYTTIT

Fig. 23Q

SsrB

MKEYKILLVDDHEIIINGIMNALLPWPBFKIVEHVKNGLLEVYNACCAYEPDILILDLSLPGINGLDIIPQLHQRPAMNI
LVYTAYQQEYMTIKTLAAGANGYVLKSSSQVLLAALQTVAVNKRIDPTLNREAILAELNADTTNHQLTLRERQVLKL
IDEGYTNHGISEKLHISIKTVETHRMNMMRKLOVHKVTELLNCARRMLIEY

Figure 24

Fig. 24A

Promoter A2

GCTTCCCTCCAGTTGCCTGTTGCAAAATCTTTGGCACTTGATCACTATCGCAGTACATATAGTTTCATCAGAAGATTAAT
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AGAGATAGTCGAAATAAATGTGAATCAGGCTTTTTACGGATGTGGTTGTGAGCGAATTTGATAGAAAC

Fig. 24B

Promoter B

TAAAAATATCTTAGAGCCTATCCCACCAGGCGTTAATTGGCGCAGCCAGTTTGGACACGGATAGCGCGCAAAAACCGCAG
CGTACACGTAGTACGTGAGGTTTGACTCGCTACGCTCGCCCTTCGGGCCGCCGCTAGCGGCGTTCAAACGCTAACGCGT
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<110> Creatogen Biosciences GmbH

<120> Carrier System for Vaccines

<130> 19130pwo carriersystem

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gca gct gca aaa gtg ctt gac tcc ggt ttt ggc gag gaa gtg gtt gag 816
cgt atg gta ggt gca ggg gaa gca gaa ata gag gag ttg gct gaa aag 864
ttt ggc gaa gaa gtg agc gaa agt ttt tcc aaa caa ttt gag ccg ctt 912
gaa cgt gaa atg gct atg gcg aat gag atg gca gag gag gct gcc gag 960
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gcc ctg gaa aaa tgt gtg caa gaa ggt gga aag ttc ctg tta aaa aaa 1104
ttc cgt aat aaa gtt ctc ttc aat atg ttc aaa aaa atc ctg tat gcc 1152
tta ctg agg gat tgt tca ttt aaa ggc tta cag gct atc aga tgt gca 1200
acc gag ggc gcc agt cag atg aat act ggc atg gtt aac aca gaa aaa 1248
gcg aag atc gaa aag aaa ata gag caa tta ata act cag caa cgg ttt 1296
ctg gat ttc ata atg caa caa aca gaa aac cag aaa aag ata gaa caa 1344
aaa cgc tta gag gag ctt tat aag ggg acg ggt gcc gcg ctt aga gat 1392
gta tta gat acc att gat cac tat agt agc gtt cag gcg aga ata gct 1440
ggc tat cgc gct taa 1455

<210> 6

<211> 504

<212> DNA

<213> Salmonella

<220>

<221> exon

<222> (1)..(501)

<400> 6

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atg ggt act gaa tca atg ctt ctg tta ttt gat gat atc tgg atg aag      48
cta atg gag ctt gcc aaa aag ctg cgc gat atc atg cgc agc tat aac      96
gta gaa aaa caa cgg ctg gcc tgg gaa ctg caa gtc aat gtt tta cag     144
acg caa atg aaa aca att gat gaa gcg ttt aga gca tca atg att act     192
gcg ggt ggc gca atg ttg tcg ggt gta ctg acg ata gga tta ggg gcc     240
gta ggc ggg gaa acc ggt ctt ata gcg ggt caa gcc gta ggc cac aca     288
gct ggg ggc gtc atg ggc ctg ggg gct ggt gta gcg caa cgt caa agt     336
gat caa gat aaa gcg att gcc gac ctg caa caa aat ggg gcc caa tct     384
tat aat aaa tcc ctg acg gaa att atg gag aaa gca act gaa att atg     432
cag caa atc atc ggc gtg ggg tcg tca ctg gtc acg gtt ctt gct gaa     480
ata ctc cgg gca tta acg agg taa                                     504

```

<210> 7

<211> 195

<212> PRT

<213> Salmonella

<400> 7

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Met Glu Ala Ser Asn Val Ala Leu Val Leu Pro Ala Pro Ser Leu Leu
 1              5              10              15
Thr Pro Ser Ser Thr Pro Ser Pro Ser Gly Glu Gly Met Gly Thr Glu
          20          25          30
Ser Met Leu Leu Leu Phe Asp Asp Ile Trp Met Lys Leu Met Glu Leu
          35          40          45
Ala Lys Lys Leu Arg Asp Ile Met Arg Ser Tyr Asn Val Glu Lys Gln
          50          55          60
Arg Leu Ala Trp Glu Leu Gln Val Asn Val Leu Gln Thr Gln Met Lys

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65		70		75		80									
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				85					90					95	
Met	Leu	Ser	Gly	Val	Leu	Thr	Ile	Gly	Leu	Gly	Ala	Val	Gly	Gly	Glu
			100					105					110		
Thr	Gly	Leu	Ile	Ala	Gly	Gln	Ala	Val	Gly	His	Thr	Ala	Gly	Gly	Val
		115					120					125			
Met	Gly	Leu	Gly	Ala	Gly	Val	Ala	Gln	Arg	Gln	Ser	Asp	Gln	Asp	Lys
		130				135					140				
Ala	Ile	Ala	Asp	Leu	Gln	Gln	Asn	Gly	Ala	Gln	Ser	Tyr	Asn	Lys	Ser
145					150					155				160	
Leu	Thr	Glu	Ile	Met	Glu	Lys	Ala	Thr	Glu	Ile	Met	Gln	Gln	Ile	Ile
				165					170					175	
Gly	Val	Gly	Ser	Ser	Leu	Val	Thr	Val	Leu	Ala	Glu	Ile	Leu	Arg	Ala
			180					185					190		
Leu	Thr	Arg													
		195													

<210> 8
 <211> 417
 <212> DNA
 <213> Salmonella

<220>
 <221> exon
 <222> (1)..(414)

<400> 8
 atg gtg caa gaa ata gag caa tgg tta cgt cgg cat cag gtg ttt act 48
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 ata tta tcg cct tac ctg gtg atc tat cgt att gag gca aaa gaa atg 144
 att att tgt gag ttc agg cgc ctg acg ccc ggg caa cct cga cca cag 192
 caa ttg ttt cac tta ctg gga ctt tta cgc ggg ata ttt gtg cat cac 240

ccg cag tta aca tgt tta aag atg ttg ata atc acc gac gtt ctg gat 288
 gaa aaa aaa gcc atg cta cgc agg aaa tta ttg cgc atc ctg aca gta 336
 atg gga gcg acc ttt aca cag ctt gat ggc gat aac tgg aca gtt tta 384
 tcc gcc gag cat ctt atc cag cga cgt ttt taa 417

<210> 9

<211> 789

<212> DNA

<213> Salmonella

<220>

<221> exon

<222> (1)..(786)

<400> 9

atg aaa att cat att ccg tca gcg gca agt aat ata gtc gat ggt aat 48
 agt cct cct tcc gat ata caa gcg aag gag gta tcg ttt cct ccc cct 96
 gaa att cca gcg cct ggc acc ccc gca gcc cct gtg ctg ctt acg cct 144
 gaa caa ata agg cag cag agg gat tat gcg ata cat ttt atg caa tac 192
 act att cgt gcg ctg ggt gcg aca gtc gtg ttt ggg tta tcg gtt gct 240
 gca gcg gta att tct ggc ggg gca gga tta ccc att gct att ctt gcg 288
 ggg gcg gcg ctc gtg att gct att ggg gat gct tgc tgt gcg tat cat 336
 aat tat caa tcg ata tgt cag caa aag gag cca tta caa acc gcc agt 384
 gat agc gtt gct ctt gtg gtc agt gcg ctg gcc tta aaa tgt ggg gca 432
 agt ctt aac tgc gct aac acc ctt gct aat tgt ctt tct tta tta ata 480
 cgt tca gga atc gct att tct atg ttg gtt tta ccc cta cag ttt cca 528
 ctg ccc gcg gct gaa aat att gcg gcc tct ttg gac atg ggg agt gta 576
 att acc tcc gtt agc ctg acg gcg ata ggt gcg gta ctg gat tat tgc 624
 ctt gcc cgc ccc tct ggc gac gat cag gaa aat tct gtt gat gaa ctt 672

cat gcc gat ccc agt gtg tta ttg gcg gaa caa atg gca gcg ctc tgt 720
 caa tct gct act aca cct gca cct gca tta atg gac agt tct gat cat 768
 aca tct cgg gga gaa cca tga 789

<210> 10
 <211> 690
 <212> DNA
 <213> Salmonella

<220>
 <221> exon
 <222> (1)..(687)

<400> 10
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 acc aat atg gag agt ggt aga ata gga cct caa caa gga aaa gag cgg 144
 gta ttg gcc gga ctt gcg aaa cga gtg ata gag tgt ttt cca aaa gaa 192
 att ttt agt tgg caa acg gtt att ttg ggc gga cag att tta tgc tgt 240
 tcc gct gga ata gca tta aca gtg cta agt ggt gga ggc gcg ccg ctc 288
 gta gcc ctg gca ggg att ggc ctt gct att gcc atc gcg gat gtc gcc 336
 tgt ctt atc tac cat cat aaa cat cat ttg cct atg gct cac gac agt 384
 ata ggc aat gcc gtt ttt tat att gct aat tgt ttc gcc aat caa cgc 432
 aaa agt atg gcg att gct aaa gcc gtc tcc ctg ggc ggt aga tta gcc 480
 tta acc gcg acg gta atg act cat tca tac tgg agt ggt agt ttg gga 528
 cta cag cct cat tta tta gag cgt ctt aat gat att acc tat gga cta 576
 atg agt ttt act cgc ttc ggt atg gat ggg atg gca atg acc ggt atg 624
 cag gtc agc agc cca tta tat cgt ttg ctg gct cag gta acg cca gaa 672
 caa cgt gcg ccg gag taa 690

<210> 11
 <211> 474
 <212> DNA
 <213> Salmonella

<220>
 <221> exon
 <222> (1)..(471)

<400> 11
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 ttc cgg cgt ggc ggc tcg ctg cgt atg ttg ttg gat gac gat gtt aca 96
 cag ccg ctt aat act ctg tat cgc tat gcc acg cag ctt atg gag gta 144
 aaa gaa ttc gcc ggc gca gcg cga ctt ttt caa ttg ctg acg ata tat 192
 gat gcc tgg tca ttt gac tac tgg ttt cgg tta ggg gaa tgc tgc cag 240
 gct caa aaa cat tgg ggg gaa gcg ata tac gct tat gga cgc gcg gca 288
 caa att aag att gat gcg ccg cag gcg cca tgg gcc gca gcg gaa tgc 336
 tat ctc gcg tgt gat aac gtc tgt tat gca atc aaa gcg tta aag gcc 384
 gtg gtg cgt att tgc ggc gag gtc agt gaa cat caa att ctc cga cag 432
 cgt gca gaa aag atg tta cag caa ctt tct gac agg agc taa 474

<210> 12
 <211> 435
 <212> DNA
 <213> Salmonella

<220>
 <221> exon
 <222> (1)..(432)

<400> 12
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 aaa cag cta tta tcc gtt gat ccg gaa acc gtt tat gcc agt ggt tac 96

gcc tca tgg cag gag ggg gat tat tcg cgc gcc gta atc gat ttt agt 144
 tgg ctg gtg atg gcc cag cca tgg agt tgg cgt gcc cat att gca ttg 192
 gct ggc acc tgg atg atg ctt aaa gaa tac acg acg gcc att aat ttc 240
 tat gga cat gcc ttg atg ctg gat gcc agc cat cca gaa ccg gtt tac 288
 caa acg ggc gtc tgt ctc aaa atg atg ggg gaa ccc ggg ttg gcg aga 336
 gag gct ttt caa acc gca atc aag atg agt tat gcg gat gcc tca tgg 384
 agt gag att cgc cag aat gcg caa ata atg gtt gat act ctt att gct 432
 taa 435

<210> 13

<211> 1212

<212> DNA

<213> Salmonella

<220>

<221> exon

<222> (1) .. (1209)

<400> 13

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 tta ggt cac gtt tta caa ggc cgg gaa gta tgg ctg aat gaa ggt aac 96
 ctg tca ctg ggg gag aag gga tgc gat att tgt att ccg ctg gct ata 144
 aat gaa aaa att att ctg aga gaa cag gca gat agt tta ttt gtt gat 192
 gcc ggg aaa gcc aga gtt aga gtt aat ggc cgc aga ttt aat cca aat 240
 aag ccg cta cca tcc agt ggg gtt ttg cag gtt gcg gga gtg gct atc 288
 gcg ttt ggt aaa cag gat tgt gaa ctt gct gat tat caa ata ccc gtt 336
 tcc aga tca ggg tac tgg tgg ttg gct ggc gta ttc ttg att ttc atc 384
 ggt gga atg ggt gtc ctg tta agt att agt ggt cag cct gaa acg gta 432
 aat gac tta cct ttg cgg gtt aag ttt tta tta gac aaa agc aat att 480

cat tat gtg cgg gcg caa tgg aaa gaa gat ggc agc ctg cag ttg tcc 528
 ggt tat tgc tcg tca agc gaa cag atg caa aag gtg aga gcg act ctc 576
 gaa tca tgg ggg gtc atg tat cgg gat ggt gta atc tgt gat gac tta 624
 ttg gta cga gaa gtg cag gat gtt ttg ata aaa atg ggt tac ccg cat 672
 gct gaa gta tcc agc gaa ggg ccg ggg agc gtg tta att cat gat gat 720
 ata caa atg gat cag caa tgg cgc aag gtt caa cca tta ctt gca gat 768
 att ccc ggg tta ttg cac tgg cag att agt cac tct cat cag tct cag 816
 ggg gat gat att att tct gcg ata ata gag aac ggt tta gtg ggg ctt 864
 gtc aat gtt agc cca atg cgg cgc tct ttt gtt atc agt ggt gta ctg 912
 gat gaa tct cat caa cgc att ttg caa gaa acg tta gca gca tta aag 960
 aaa aag gat ccc gct ctt tct tta att tat cag gat att gcg cct tcc 1008
 cat gat gaa agc aag tat ctg cct gcg cca gtg gct ggc ttt gta cag 1056
 agt cgc cat ggt aat tac tta tta ctg acg aat aaa gag cgt tta cgt 1104
 gta ggg gca ttg tta ccc aat ggg gga gaa att gtc cat ctg agt gcc 1152
 gat gtg gta acg att aaa cat tat gat act ttg att aac tat cca tta 1200
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<210> 14

<211> 243

<212> DNA

<213> Salmonella

<220>

<221> exon

<222> (1) .. (240)

<400> 14

atg aca act ttg acc cgg tta gaa gat ttg ctg ctt cat tcg cgt gaa 48
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gaa gag aac aac ggc aag tta cag gat ccg cag caa tat cag caa aac 144
 acc tta ttg ctt gaa gcg atc gag cag gcc gaa aat atc atc aac att 192
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 taa 243

<210> 15
 <211> 216
 <212> DNA
 <213> Salmonella

<220>
 <221> exon
 <222> (1)..(213)

<400> 15
 atg gat att gca caa tta gtg gat atg ctc tcc cac atg gcg cac cag 48
 gca ggc cag gcc att aat gac aaa atg aat ggt aat gat ttg ctc aac 96
 cca gaa tcg atg att aaa gcg caa ttt gcc tta cag cag tat tct aca 144
 ttt att aat tac gaa agt tca ctg atc aaa atg atc aag gat atg ctt 192
 agt gga atc att gct aaa atc tga 216

<210> 16
 <211> 228
 <212> DNA
 <213> Salmonella

<220>
 <221> exon
 <222> (1)..(225)

<400> 16
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 tgt ctg gca tta ttg ttg gcg ggt tta aat gag ccg cta aaa gcc gcg 144

aaa att tta tcg gat ata gat ttg cca gag gct atg gcg ctg cgt ctg 192

tta ttt cct gca cca aat gag ggg ttt gaa aat tga 228

<210> 17

<211> 249

<212> DNA

<213> Salmonella

<220>

<221> exon

<222> (1)..(246)

<400> 17

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gaa ccg agc cag gag caa att aat ttt ttt gaa caa ttg ctg aaa gat 96

gaa gca tcc acc agt aac gcc agt gct tta tta ccg cag gtt atg ttg 144

acc aga caa atg gat tat atg cag tta acg gta ggc gtc gat tat ctt 192

gcc aga ata tca ggc gca gca tcg caa gcg ctt aat aag ctg gat aac 240

atg gca tga 249

<210> 18

<211> 750

<212> DNA

<213> Salmonella

<220>

<221> exon

<222> (1)..(747)

<400> 18

atg aag gtt cat cgt ata gta ttt ctt act gtc ctt acg ttc ttt ctt 48

acg gca tgt gat gtg gat ctt tat cgc tca ttg cca gaa gat gaa gcg 96

aat caa atg ctg gca tta ctt atg cag cat cat att gat gcg gaa aaa 144

aaa cag gaa gag gat ggt gta acc tta cgt gtc gag cag tcg cag ttt 192

att aat gcg gtt gag cta ctt aga ctt aac ggt tat ccg cat agg cag 240
 ttt aca acg gcg gat aag atg ttt ccg gct aat cag tta gtg gta tca 288
 ccc cag gaa gaa cag cag aag att aat ttt tta aaa gaa caa aga att 336
 gaa gga atg ctg agt cag atg gag ggc gtg att aat gca aaa gtg acc 384
 att gcg cta ccg act tat gat gag gga agt aac gct tct ccg agc tca 432
 gtt gcc gta ttt ata aaa tat tca cct cag gtc aat atg gag gcc ttt 480
 cgg gta aaa att aaa gat tta ata gag atg tca atc cct ggg ttg caa 528
 tac agt aag att agt atc ttg atg cag cct gct gaa ttc aga atg gta 576
 gct gac gta ccc gcg aga caa aca ttc tgg att atg gac gtt atc aac 624
 gcc aat aaa ggg aag gtg gtg aag tgg ttg atg aaa tac cct tat ccg 672
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 ggc tat ttt tgc ctg aga cgc cgt ttt tga 750

<210> 19

<211> 2763

<212> DNA

<213> Salmonella

<220>

<221> exon

<222> (1) .. (2760)

<400> 19

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 tct gtg ctt acc gca gct tat ata tca atg gtt cag aaa cgg cag cat 144
 ata ata gag gat tta tcc gtt cta tcc gag atg aat att gta cta agc 192
 aat caa cgg ttt gaa gaa gct gaa cgt gac gct aaa aat tta atg tat 240
 caa tgc tca tta gcg act gag att cat cat aac gat att ttc cct gag 288

gtg agc cgg cat cta tct gtc ggt cct tca aat tgc acg ccg acg cta 336
 aac gga gag aag cac cgt ctc ttt ctg cag tcc tct gat atc gat gaa 384
 aat agc ttt cgt cgc gat agt ttt att ctt aat cat aaa aat gag att 432
 tcg tta tta tct act gat aac cct tca gat tat tca act cta cag cct 480
 tta acg cga aaa agc ttt cct tta tac cca acc cat gcc ggg ttt tac 528
 tgg agt gaa cca gaa tac ata aac ggc aaa gga tgg cac gct tcc gtt 576
 gcg gtt gcc gat cag caa ggc gta ttt ttt gag gtg acg gtt aaa ctt 624
 ccc gat ctc att act aag agc cac ctg cca tta gat gat agt att cga 672
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 gca aaa aaa cgc gct gag cga gct aac aaa cgt aaa agc att cat ctt 1200
 acg gta ata agt cat gag tta cgt act ccg atg aat ggc gta ctc ggt 1248
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acc atc cag ggg cca gcg caa agc aaa aaa ctg tca tta cgt act ttt 1488
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cgg caa att ttg gtt aat tta ctc ggg aac gcg gta aaa ttt acc gaa 1584
acc gga ggg ata cgt ctg acg gtc aag cgt cat gag gaa caa tta ata 1632
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aat ctg aca cta aaa agt gtc ccc ggg gtt gga acc tgt gtc tcg cta 1824
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ctg tca gcg ccg ttc tgc ctg cat cgg caa ctg gct tgc tgg gga ata 1920
cgc ggt gaa cca ccc cac cag caa aat gcg ctt ctc aac gca gag ctt 1968
ttg tat ttc tcc gga aaa ctc tac gac ctg gcg caa cag tta ata ttg 2016
tgt aca cca aat atg cca gta ata aat aat ttg tta cca ccc tgg cag 2064
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ctg att gac att aga atg cca gaa ata gat ggt att gaa tgt gta cga 2256
tta tgg cat gat gag ccg aat aat tta gat cct gac tgc atg ttt gtg 2304
gca cta tcc gct agc gta gcg aca gaa gat att cat cgt tgt aaa aaa 2352
aat ggg att cat cat tac att aca aaa cca gtg aca ttg gct acc tta 2400
gct cgc tac atc agt att gcc gca gaa tac caa ctt tta cga aat ata 2448
gag cta cag gag cag gat ccg agt cgc tgc tca gcg cta ctg gcg aca 2496
gat gat atg gtc att aat agc aag att ttc caa tca ctg gac ctc ttg 2544
ctg gct gat att gaa aat gcc gta tcg gct gga gaa aaa atc gat cag 2592

tta att cac aca tta aaa ggc tgt tta ggt caa ata ggg cag act gaa 2640
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 atc atc gcg ctg gag gaa cta acc gac tta cgc cag aaa ata cgt atg 2736
 atc ttc aaa aac tac acc att act taa 2763

<210> 20
 <211> 639
 <212> DNA
 <213> Salmonella

<220>
 <221> exon
 <222> (1)..(636)

<400> 20
 atg aaa gaa tat aag atc tta tta gta gac gat cat gaa atc atc att 48
 aac ggc att atg aat gcc tta tta ccc tgg cct cat ttt aaa att gta 96
 gag cat gtt aaa aat ggt ctt gag gtt tat aat gcc tgt tgt gca tac 144
 gag cct gac ata ctt atc ctt gat ctt agt cta cct ggc atc aat ggc 192
 ctg gat atc att cct caa tta cat cag cgt tgg cca gca atg aat att 240
 ctg gtt tac aca gca tac caa caa gag tat atg acc att aaa act tta 288
 gcc gca ggt gct aat ggc tat gtt tta aaa agc agt agt cag caa gtt 336
 ctg tta gcg gca ttg caa aca gta gca gta aac aag cgt tac att gac 384
 cca acg ttg aat cgg gaa gct atc ctg gct gaa tta aac gct gac acg 432
 acc aat cat caa ctg ctt act ttg cgc gag cgt cag gtt ctt aaa ctt 480
 att gac gag ggg tat acc aat cat ggg atc agc gaa aag cta cat atc 528
 agt ata aaa acc gtc gaa aca cac cgg atg aat atg atg aga aag cta 576
 cag gtt cat aaa gtg aca gag tta ctt aac tgt gcc cga aga atg agg 624
 tta ata gag tat taa 639

<210> 21
 <211> 388
 <212> DNA
 <213> Salmonella

<400> 21
 gcttccctcc agttgcctgt tgcaaaatct ttggcacttg atcactatcg cagtacatat 60
 agtttcatca gaagattaat cgatgggtgtt atcattagga agataaattt cttcatatat 120
 aaccagtcg atgactacaa ttacttttta ataagatggc gatgtaaaaa catcgtaaca 180
 gtttatttaa taaataattt ttcaaattgt aagtttttat gtcaatgctg aaaatgtaat 240
 tgtgaattta tcggaaaatc cgaatgatag aatcgctgt gacaaggat atgtagacag 300
 catcctgata ttgtacaaga agagatagtc gaaataaatg tgaatcaggc tttttacgga 360
 tgtggtgtg agcgaatttg atagaaac 388

<210> 22
 <211> 262
 <212> DNA
 <213> Salmonella

<400> 22
 taaaaatattc ttagagccta tcccaccagg cgtaattgg cgcagccagt ttggacacgg 60
 atagcgcgca aaaaccgcag cgtacacgta gtacgtgagg ttgactcgc tacgctcgcc 120
 cttcggggccg ccgctagcgg cgttcaaaac gtaacgcgt ttggcgagc actgccagg 180
 ttcaaaatgg caagtaaaat agcctaattg gataggctct tagttagcac gttaattatc 240
 tatcgtgtat atggagggga at 262

<210> 23
 <211> 192
 <212> PRT
 <213> EPEC

<300>
 <303> Mol. Microbiol.
 <304> 28
 <306> 1-4
 <307> 1998

<400> 23
 Met Asp Thr Ser Thr Thr Ala Ser Val Ala Ser Ala Asn Ala Ser Thr
 1 5 10 15
 Ser Thr Ser Met Ala Tyr Asp Leu Gly Ser Met Ser Lys Asp Asp Val
 20 25 30

Ile Asp Leu Phe Asn Lys Leu Gly Val Phe Gln Ala Ala Ile Leu Met
 35 40 45
 Phe Ala Tyr Met Tyr Gln Ala Gln Ser Asp Leu Ser Ile Ala Lys Phe
 50 55 60
 Ala Asp Met Asn Glu Ala Ser Lys Glu Ser Thr Thr Ala Gln Lys Met
 65 70 75 80
 Ala Asn Leu Val Asp Ala Lys Ile Ala Asp Val Gln Ser Ser Ser Asp
 85 90 95
 Lys Asn Ala Lys Ala Gln Leu Pro Asp Glu Val Ile Ser Tyr Ile Asn
 100 105 110
 Asp Pro Arg Asn Asp Ile Thr Ile Ser Gly Ile Asp Asn Ile Asn Ala
 115 120 125
 Gln Leu Gly Ala Gly Asp Leu Gln Thr Val Lys Ala Ala Ile Ser Ala
 130 135 140
 Lys Ala Asn Asn Leu Thr Thr Thr Val Asn Asn Ser Gln Leu Glu Ile
 145 150 155 160
 Gln Gln Met Ser Asn Thr Leu Asn Leu Leu Thr Ser Ala Arg Ser Asp
 165 170 175
 Met Gln Ser Leu Gln Tyr Arg Thr Ile Ser Gly Ile Ser Leu Gly Lys
 180 185 190

<210> 24
 <211> 380
 <212> PRT
 <213> EPEC

<300>
 <303> Mol. Microbiol.
 <304> 28
 <306> 1-4
 <307> 1998

<400> 24
 Met Leu Asn Val Asn Asn Asp Ile Gln Ser Val Arg Ser Gly Ala Ser

1	5	10	15
Ala Ala Thr	Ala Thr Ser Gly Ile Asn Gln Ser Glu Val Thr Ser Ala		
	20	25	30
Leu Asp Leu Gln Leu Val Lys Ser Thr Ala Pro Ser Ala Ser Trp Thr			
	35	40	45
Glu Ser Thr Ala Leu Ala Thr Pro Pro Ala Gly His Ser Leu Val Thr			
	50	55	60
Pro Ser Ala Ala Glu Asp Val Leu Ser Lys Leu Phe Gly Gly Ile Ser			
	65	70	75
Gly Glu Val Thr Ser Arg Thr Glu Gly Thr Glu Pro Gln Arg Ser Thr			
	85	90	95
Gln Asn Ala Ser Ser Gly Tyr Pro Tyr Leu Ser Gln Val Asn Asn Val			
	100	105	110
Asp Pro Gln Ala Met Met Met Met Ala Thr Leu Leu Ser Leu Asp Ala			
	115	120	125
Ser Ala Gln Arg Val Ala Ser Met Lys Asn Ser Asn Glu Ile Tyr Ala			
	130	135	140
Asp Gly Gln Asn Lys Ala Leu Asp Asn Lys Thr Leu Glu Phe Lys Lys			
	145	150	155
Gln Leu Glu Glu Gln Gln Lys Ala Glu Glu Lys Ala Gln Lys Ser Lys			
	165	170	175
Ile Val Gly Gln Val Phe Gly Trp Leu Gly Val Ala Ala Thr Ala Ile			
	180	185	190
Ala Ala Ile Phe Asn Pro Ala Leu Trp Ala Val Val Ala Ile Ser Ala			
	195	200	205
Thr Ala Met Ala Leu Gln Thr Ala Val Asp Val Met Gly Asp Asp Ala			
	210	215	220
Pro Gln Ala Leu Lys Thr Ala Ala Gln Ala Phe Gly Gly Leu Ser Leu			
	225	230	235
Ala Ala Gly Ile Leu Thr Ala Gly Ile Gly Gly Val Ser Ser Leu Ile			
	245	250	255
Ser Lys Val Gly Asp Val Ala Asn Lys Val Gly Ser Asn Ile Val Lys			

260	265	270
Val Val Thr Thr Leu Ala Asp Thr Phe Val Asp Asn Val Ala Ser Lys		
275	280	285
Ile Ser Ala Val Ala Asn Gly Leu Thr Thr Ser Ser Arg Ser Ile Gly		
290	295	300
Thr Thr Val Leu Asn Asn Asp Ala Ala Tyr Tyr Asn Val Leu Ser Gln		
305	310	315
Val Ser Ala Phe Ala Val Glu Asn Leu Thr Arg Gln Ser Glu Tyr Leu		
325	330	335
Ser Gln Ser Ala Lys Ala Glu Leu Glu Lys Ala Thr Leu Glu Leu Gln		
340	345	350
Asn Gln Ala Asn Tyr Ile Gln Ser Ala Ser Gln Leu Met Ser Asp Ser		
355	360	365
Ala Arg Val Asn Ile Arg Ile Val Ser Gly Arg Val		
370	375	380

<210> 25
 <211> 401
 <212> PRT
 <213> Yersinia enterocolitica

<300>
 <301> Hakansson, S.
 Schesser, K.
 Persson, C.
 Galyov, E. E.
 Rosqvist, R.
 Hornble, F.
 Wolf Watz, H.
 <303> EMBO J.
 <304> 15
 <306> 5812-5823
 <307> 1996

<400> 25
 Met Ser Ala Leu Ile Thr His Asp Arg Ser Thr Pro Val Thr Gly Ser
 1 5 10 15

Leu Val Pro Tyr Ile Glu Thr Pro Ala Pro Ala Pro Leu Gln Thr Gln

20	25	30
Gln Val Ala Gly Glu Leu Lys Asp Lys Asn Gly Gly Val Ser Ser Gln		
35	40	45
Gly Val Gln Leu Pro Ala Pro Leu Ala Val Val Ala Ser Gln Val Thr		
50	55	60
Glu Gly Gln Gln Gln Glu Ile Thr Lys Leu Leu Glu Ser Val Thr Arg		
65	70	75
80		
Gly Thr Ala Gly Ser Gln Leu Ile Ser Asn Tyr Val Ser Val Leu Thr		
85	90	95
Asn Phe Thr Leu Ala Ser Pro Asp Thr Phe Glu Ile Glu Leu Gly Lys		
100	105	110
Leu Val Ser Asn Leu Glu Glu Val Arg Lys Asp Ile Lys Ile Ala Asp		
115	120	125
Ile Gln Arg Leu His Glu Gln Asn Met Lys Lys Ile Glu Glu Asn Gln		
130	135	140
Glu Lys Ile Lys Glu Thr Glu Glu Asn Ala Lys Gln Val Lys Lys Ser		
145	150	155
160		
Gly Met Ala Ser Lys Ile Phe Gly Trp Leu Ile Ala Ile Ala Ser Val		
165	170	175
Val Ile Gly Ala Ile Met Val Ala Ser Gly Val Gly Ala Val Ala Gly		
180	185	190
Ala Met Met Ile Ala Ser Gly Val Ile Gly Met Ala Asn Met Ala Val		
195	200	205
Lys Gln Ala Ala Glu Asp Gly Leu Ile Ser Gln Glu Ala Met Gln Val		
210	215	220
Leu Gly Pro Ile Leu Thr Ala Ile Glu Val Ala Leu Thr Val Val Ser		
225	230	235
240		
Thr Val Met Thr Phe Gly Gly Ser Ala Leu Lys Cys Leu Ala Asp Ile		
245	250	255
Gly Ala Lys Leu Gly Ala Asn Thr Ala Ser Leu Ala Ala Lys Gly Ala		
260	265	270
Glu Phe Ser Ala Lys Val Ala Gln Ile Ser Thr Gly Ile Ser Asn Thr		

275	280	285
Val Gly Ser Ala Val Thr Lys Leu Gly Gly Ser Phe Gly Ser Leu Thr		
290	295	300
Met Ser His Val Ile Arg Thr Gly Ser Gln Ala Thr Gln Val Ala Val		
305	310	315 320
Gly Val Gly Ser Gly Ile Thr Gln Thr Ile Asn Asn Lys Lys Gln Ala		
325	330	335
Asp Leu Gln His Asn Asn Ala Asp Leu Ala Leu Asn Lys Ala Asp Met		
340	345	350
Ala Ala Leu Gln Ser Ile Ile Asp Arg Leu Lys Glu Glu Leu Ser His		
355	360	365
Leu Ser Glu Ser His Arg Gln Val Met Glu Leu Ile Phe Gln Met Ile		
370	375	380
Asn Ala Lys Gly Asp Met Leu His Asn Leu Ala Gly Arg Pro His Thr		
385	390	395 400

Val

<210> 26
 <211> 390
 <212> PRT
 <213> Pseudomonas aeruginosa

<300>
 <301> Hauser, A. R.
 Fleiszig, S.
 Kang, P. J.
 Mostov, K.
 Engel, J. N.
 <303> Infect. Immun.
 <304> 66
 <306> 1413-1420
 <307> 1998

<400> 26
 Met Asn Pro Ile Thr Leu Glu Arg Ala Gly Leu Pro Tyr Gly Val Ala
 1 5 10 15

Asp Ala Gly Asp Ile Pro Ala Leu Gly Arg Pro Val Ala Arg Asp Val
 20 25 30

Glu Ser Leu Arg Val Glu Arg Leu Ala Ala Pro Ala Ala Ala Ser Ala
 35 40 45

Ser Gly Thr Gly Val Ala Leu Thr Pro Pro Ser Ala Ala Ser Gln Gln
 50 55 60

Arg Leu Glu Val Ala Asn Arg Ala Glu Ile Ala Ser Leu Val Gln Ala
 65 70 75 80

Val Gly Glu Asp Ala Gly Leu Ala Arg Gln Val Val Leu Ala Gly Ala
 85 90 95

Ser Thr Leu Leu Ser Ala Gly Leu Met Ser Pro Gln Ala Phe Glu Ile
 100 105 110

Glu Leu Ala Lys Ile Thr Gly Glu Val Glu Asn Gln Gln Lys Lys Leu
 115 120 125

Lys Leu Thr Glu Ile Glu Gln Ala Arg Lys Gln Asn Leu Gln Lys Met
 130 135 140

Glu Asp Asn Gln Gln Lys Ile Arg Glu Ser Glu Glu Ala Ala Lys Glu
 145 150 155 160

Ala Gln Lys Ser Gly Leu Ala Ala Lys Ile Phe Gly Trp Ile Ser Ala
 165 170 175

Ile Ala Ser Ile Ile Val Gly Ala Ile Met Val Ala Thr Gly Val Gly
 180 185 190

Ala Ala Ala Gly Ala Leu Met Ile Ala Gly Gly Val Met Gly Val Val
 195 200 205

Ser Gln Ser Val Gln Gln Ala Ala Ala Asp Gly Leu Ile Ser Lys Glu
 210 215 220

Val Met Glu Lys Leu Gly Pro Ala Leu Met Gly Ile Glu Ile Ala Val
 225 230 235 240

Ala Leu Leu Ala Ala Val Val Ser Phe Gly Gly Ser Ala Val Gly Gly
 245 250 255

Leu Ala Lys Leu Gly Ala Lys Ile Gly Gly Lys Ala Ala Glu Met Thr
 260 265 270

Ala Ser Leu Ala Ser Lys Val Ala Asn Leu Gly Gly Lys Phe Gly Ser
 275 280 285

Leu Ala Gly Gln Ser Leu Ser His Ser Leu Lys Leu Gly Val Gln Val
 290 295 300

Ser Asp Leu Thr Leu Asp Val Ala Asn Gly Ala Ala Gln Ala Thr His
 305 310 315 320

Ser Gly Phe Gln Ala Lys Ala Ala Asn Arg Gln Ala Asp Val Gln Glu
 325 330 335

Ser Arg Ala Asp Leu Thr Thr Leu Gln Gly Val Ile Glu Arg Leu Lys
 340 345 350

Glu Glu Leu Ser Arg Met Leu Glu Ala Phe Gln Glu Ile Met Glu Arg
 355 360 365

Ile Phe Ala Met Leu Gln Ala Lys Gly Glu Thr Leu His Asn Leu Ser
 370 375 380

Ser Arg Pro Ala Ala Ile
 385 390

<210> 27
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 27
 tttttacgtg aagcggggtg

20

<210> 28
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 28
 ggcattagcg gatgtctgac tg

22

<210> 29
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 29
caccaggaac cattttctct gg

22

<210> 30
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 30
cagcgatgac gatattcgac aag

23

<210> 31
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 31
gaaatcccgc agaaatg

17

<210> 32
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 32
aaggcgataa tataaac

17

<210> 33
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 33
agagatgtat tagatac

17

<210> 34
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 34
gcaataagag tatcaac

17

<210> 35
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 35
gctaagcttc ggctcaaatt gtttggaana c

31

<210> 36
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 36
gctaagctta gagatgtatt agatacc

27

<210> 37
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 37
attggatccg caagcgtcca gaa

23

<210> 38
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 38
tatggatcct cagattaagc gcg

23

<210> 39
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 39
atagaattcg gagggagatg gattggaag

29

<210> 40
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 40
atagaattcg aagataaagc gattgccgac

30

<210> 41
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 41
gaaggatcca ctccatctcc ctc

23

<210> 42
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 42
gaaggatcca ttgctctat ttcttgc

27

<210> 43
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 43
atgggatccg agattcgcca gaatgcgcaa

30

<210> 44
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 44
atgggatcca ctggcataaa cggtttccgg

30

<210> 45
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 45
attggatcct gacgtaaadc attatca

27

<210> 46
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 46
attggatcct taagcaataa gtgaatc

27

<210> 47
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 47
aaggaattca acaggcaact ggagg

25

<210> 48
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 48
ctgccctcgc gaaaattaag ataata

26